

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 21:10:28 ; Search time 11 Seconds

(without alignments)
222.464 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59

Sequence: 1 KYHGSILARAGKVRGQTPKVA.....RRFVNVVPTFGKKKGPANNS 59

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 segs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	59	RS30_HUMAN	Q05472 homo sapien
2	22	37.3	62	RS30_ARATH	P49689 arabidopsis
3	18	30.5	59	RS30_ORYLA	O9W690 oryzias lat
4	12	20.3	58	RS30_PLAFA	O96269 plasmodium
5	12	20.3	61	RS30_SCHPO	O42952 schizosacch
6	12	20.3	62	RS30_YEAST	Q12087 saccharomyc
7	11	18.6	11	RS30_ONCMY	P83328 oncorhynch
8	7	11.9	133	HNS_PROVU	P18818 proteus vul
9	7	11.9	346	YOC2_CAEEL	O09261 caenorhabd1
10	7	11.9	489	CO1B_HUMAN	O9hr76 homo sapien
11	7	11.9	1254	POLS_EEYVM	P36321 venezuelan
12	6	10.2	78	R27A_DICDI	P14797 dictyostell
13	6	10.2	78	RS18_BACSU	P21475 bacillus su
14	6	10.2	80	EX75_VIBCH	O9Kt11 vibrio chol
15	6	10.2	105	YGRM_MICEC	P24621 micromonos
16	6	10.2	105	YGRM_MICEC	P24621 micromonos
17	6	10.2	123	RL19_TREPA	O83879 treponema p
18	6	10.2	125	RS25_HUMAN	P25111 homo sapien
19	6	10.2	127	RS11_RICPR	O9ZCS8 rickettsia
20	6	10.2	128	YQ82_CAEEL	O09237 caenorhabd1
21	6	10.2	130	YNO3_YEAST	P53908 saccharomyc
22	6	10.2	137	YKDI_YEAST	P36098 saccharomyc
23	6	10.2	142	RS16_CANAL	O94017 candida alb
24	6	10.2	142	RS16_YEAST	P40213 saccharomyc
25	6	10.2	157	ENDY_BP4	P13340 bacterioph
26	6	10.2	175	YK20_YEAST	P36133 saccharomyc
27	6	10.2	175	RL14_LEIDO	O25278 leishmania
28	6	10.2	178	FXYS_MOUSE	P97808 mus musculu
29	6	10.2	188	CC42_CAEEL	O05062 caenorhabd1
30	6	10.2	188	RASK_CAEEL	P79800 melegaris g
31	6	10.2	195	PAPH_ECOLI	P07111 escherichia
32	6	10.2	195	PRSH_ECOLI	P42185 escherichia
33	6	10.2	198	RMRP_YEAST	P40993 saccharomyc

ALIGNMENTS

RESULT 1					ALIGNMENTS				
ID	RS30_HUMAN	STANDARD:	PRT:	59 AA.					
AC	Q05472; 095261;								O14807 homo sapien
DT	01-JUN-1994 (Rel. 29, Created)								O08989 mus musculu
DT	01-JUN-1994 (Rel. 29, Last sequence update)								P97538 rattus norv
DT	16-OCT-2001 (Rel. 40, Last annotation update)								P57212 buchmera ap
DE	40S ribosomal protein S30.								P06780 saccharomyc
GN	FAU.								P24536 burkholderi
OS	Homo sapiens (human),								P38978 hydra atten
OS	Mus musculus (mouse),								P35536 bacillus su
OS	Rattus norvegicus (Rat),								P57280 buchmera ap
OS	Cricetulus griseus (Chinese hamster), and								O8ZT21 pyrobaculum
OS	Sus scrofa (Pig).								P47006 saccharomyc
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								O94051 caenorhabd1
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
OX	NCBI_TaxID=9606, 10090, 10116, 10029, 9823;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=Human;								
RX	MEDLINE=92412144; Pubmed=1326960;								
RA	Kas K., Michiels L., Merregaert J.;								
RT	"Genomic structure and expression of the human fau gene: encoding the								
RL	ribosomal protein S30 fused to a ubiquitin-like protein.";								
RN	Biochem. Biophys. Res. Commun. 187:927-933(1992).								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=Human, and Mouse;								
RX	MEDLINE=93368957; Pubmed=8395683;								
RA	Michiels L., van der Raaijlaert E., van Hasselt F., Kas K.,								
RT	Merregaert J.;								
RL	"fau cDNA encodes a ubiquitin-like-S30 fusion protein and is								
RT	expressed as an antisense sequence in the Finkel-Biskis-Reilly murine								
RL	sarcoma virus.";								
RN	Oncogene 8:2537-2546(1993).								
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.								
RC	SPECIES=rat; STRAIN=Sprague-Dawley; TISSUE=liver;								
RX	MEDLINE=93352612; Pubmed=8394356;								
RA	Olivera J., Wool I.G.;								
RT	"The carboxyl extension of a ubiquitin-like protein is rat ribosomal								
RL	protein S30.";								
RN	J. Biol. Chem. 268:17967-17974(1993).								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=mouse; STRAIN=BA1B/c;								
RX	MEDLINE=95241522; Pubmed=7724584;								
RA	Nakamura M., Xavier R.M., Tsunematsu T., Tanigawa Y.;								
RT	"Molecular cloning and characterization of a cDNA encoding monoclonal								
RL	nonspecific suppressor factor.";								
RN	Proc. Natl. Acad. Sci. U.S.A. 92:3463-3467(1995).								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=mouse; STRAIN=BA1B/c; TISSUE=liver;								
RX	MEDLINE=95293388; Pubmed=7774934;								
RA	Castels D., Pollier C., Guenet J.-L., Merregaert J.;								

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RT "the mouse Fau gene: genomic structure, chromosomal localization, and
RT characterization of two retropseudogenes."
RL Genomics 25:291-294(1995).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=C.griseus;
RA Rossmen T.G., Wang Z.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=fig; TISSUE=uterus;
RA MEDLINE=9724440; PubMed=9089280;
RT "Diquitin is physiologically induced by interferons in luminal
RT epithelium of porcine uterine endometrium in early pregnancy: global
RT RT-PCR cDNA in place of RNA for differential display screening.";
RL FEBS Lett. 405:148-152(1997).
CC -1 MISCELLANEOUS: THIS RIBOSOMAL PROTEIN IS SYNTHESIZED AS A
CC C-TERMINAL EXTENSION PROTEIN (CEP) OF A UBQUITIN-LIKE PROTEIN.
CC -1 SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: X65921; CAA46714.1; ALT_INIT.
DR EMBL: X65923; CAA46716.1; ALT_INIT.
DR EMBL: X62671; CAA44546.1; -.
DR EMBL: X62671; CAA44545.1; ALT_INIT.
DR EMBL: X65922; CAA46715.1; ALT_INIT.
DR EMBL: D26610; BAA05655.1; ALT_INIT.
DR EMBL: L33715; AAA91564.1; ALT_INIT.
DR EMBL: U41499; AAA83776.1; ALT_INIT.
DR EMBL: U72543; AAB52915.1; ALT_INIT.
DR PIR: JCI278; JCI278.
DR Genew: HGNC:3597; FAU.
DR MIM: 134690; -.
DR MGD: MGI:102547; Fau.
DR RIBOSOMAL PROTEIN.
SQ SEQUENCE 59 AA; 6648 MW; 012AC1FB55B01A4 CRC64;
QY 1 KVGSLARAGKVRGQTPKVAKKKKRGRARRMQYNRRFNVVPTFGKKKGPANNS 59
DB 1 KVGSLARAGKVRGQTPKVAKKKKRGRARRMQYNRRFNVVPTFGKKKGPANNS 59
Query Match 100.0%; Score 59; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.2e-53;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVGSLARAGKVRGQTPKVAKKKKRGRARRMQYNRRFNVVPTFGKKKGPANNS 59
DB 1 KVGSLARAGKVRGQTPKVAKKKKRGRARRMQYNRRFNVVPTFGKKKGPANNS 59
RESULT 2
ID RS30_ARATH STANDARD; PRT; 62 AA.
AC P49689; O82203; O9MOE4;
DT 01-FEB-1996 (Rel. 33. Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S30.
GN (RPS30A OR ATG219750 OR F6P22.22) AND
GN (RPS30B OR ATG29390 OR F17A13.210) AND
GN (RPS30C OR ATG56670 OR M1K19.12).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;

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RA Lebas M., Regad F., Lescure B.;
RA Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
RL [2]
RN [2]
RP SEQUENCE FROM N.A. (RPS30A).
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buehl K.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umeyam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carreira A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Niernm W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [3]
RP SEQUENCE FROM N.A. (RPS30B).
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Meyer K.F.X., Schueller C., Mamputt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoerge W., Brandt P., Grivall L.A., Kieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheinl T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohenseil J., Zimmermann W., Weiler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schuren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastlaens I., Aert R., Defoor E.,
RA Weltenegeer T., Bothe G., Rampsperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveren M., Dirke P.,
RA Moilman P., Klein lankhorst R., Rose M., Hauf J., Koeter P.,
RA Bernseiser S., Hempel S., Feldpausch M., Lamberth R., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay R., Mayes R.,
RA Pectet A., Rajandream J., Hall S., Kay M., Lennard N., McIay R., Mayes R.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Faltmann B., Grandert R., Plavandl A.,
RA Neumann S., Argirou A., Vitale D., Ligotelli K., Dauner D., Herzi A.,
RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chetior F., Cooke R., Berger C., Montfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bleike C.,
RA Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedha N., Gnoj L., Schult K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Dione K., Cotton M., Joshi C.,
RA Antonoli B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vill D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Gill S.,
RA Grinat S., Shohdy N., Hasegawa A., Rodriguez M., Hoffman J., Gill S.,
RA Chen E., Maria M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:765-777(1999).
RN [4]
RP SEQUENCE FROM N.A. (RPS30C).
RC STRAIN=cv. Columbia;
RX MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;

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RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Sequence features of the regions of 1,367,185 bp covered by 19
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:203-216(1998).
[5]
RN SEQUENCE FROM N.A.
RC STRAIN-CV, Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/RGCRC).";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: Z26869; CAA81482.1; -;
DR EMBL: AC005169; AAC62141.2; -;
DR EMBL: AL161574; CAB79697.1; -;
DR EMBL: AL096692; -; NOT_ANNOTATED_CDS.
DR EMBL: AB013392; BAB09885.1; -;
DR EMBL: AY052341; AAK96533.1; -;
DR EMBL: AY061910; AAL31237.1; -;
KW Ribosomal protein; Multigene family.
FT CONFLICT 17 19 QTP -> RHQ (IN REF. 1).
SQ SEQUENCE 62 AA: 6887 MW: 9508F3EB72F53F33 CRC64;

Query Match 37.3%; Score 22; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 9.7e-16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGLARAGVRCGTPKVAQ 22
Db 3 KVHGLARAGVRCGTPKVAQ 24
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ID RS30_ORYLA STANDARD: PRT; 59 AA.
AC Q9M6Y0:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S30.
GN FAU OR RPS30.
OS Oryzias latipes (Medaka fish) (Japanese ricefish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthopterygii; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20070552; PubMed=10603084;
RA Henrich T., Witbrodt J.;
RT "An in situ hybridization screen for the rapid isolation of
RT differentially expressed genes.";
RL Dev. Genes Evol. 210:28-33(2000).
CC -1- MISCELLANEOUS: THIS RIBOSOMAL PROTEIN IS SYNTHESIZED AS A
CC C-TERMINAL EXTENSION PROTEIN (CEP) OF A UBIQUITIN-LIKE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: AJ238274; CAB40969.1; ALT_INIT.
KW Ribosomal protein.
SQ SEQUENCE 59 AA: 6660 MW: E91B9C088C7772CF CRC64;

Query Match 30.5%; Score 18; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 QYNRRFVNVVPFGKKG 54
Db 37 QYNRRFVNVVPFGKKG 54
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ID RS30_PLAFA STANDARD: PRT; 58 AA.
AC Q96269;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 40S ribosomal protein S30.
GN RPS30 OR PFB0885W.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99021743; PubMed=9804551;
RA Gardner M.J., Tettelin H., Carnuci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shalloo S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Science 282:1126-1132(1998).
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CC -----
DR EMBL: AE001422; AAC71966.1; -;
KW Ribosomal protein.
SQ SEQUENCE 58 AA: 6488 MW: 525675AE74D04F5F CRC64;

Query Match 20.3%; Score 12; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGLARAGV 12
Db 3 KVHGLARAGV 14
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ID RS30_SCHPO STANDARD: PRT; 61 AA.
AC Q42952; 014314;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S30.
GN (RPS30A OR RPS30 OR SPAC19812.04) OR (RPS30B OR SPBC1967.03C).
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Leneers G., Perret E., Bonnet C., Caput D., Picard A.;
 RT "Transcription of ribosomal genes is down regulated by ammonium
 starvation in fission yeast."
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (RPS30A AND RPS30B).
 RC STRAIN=972;
 RX MEDLINE=21849401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voicakeert G., Aert R., Robben J., Grymponprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Scheefel M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Egger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaue J., Motier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallade V.A., Garzon A., Thode G.,
 RA Dague R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Mture 415:871-880(2002).
 CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR S30 IN S. POMBE.
 CC -1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL: AJ002731; CA05693.1; -;
 DR EMBL: AL390814; CAC00552.1; -;
 DR EMBL: AL021839; CAA17057.2; -;
 KM Ribosomal protein; Multigene family.
 SQ SEQUENCE 61 AA; 6910 MW; 4B9C171F1A326F22 CRC64;
 QY 1 KVHGSIRAGKV 12
 DB 3 KVHGSIRAGKV 14
 RESULT 6
 RS30_YEAST STANDARD; PRT; 62 AA.
 ID RS30_YEAST
 AC 012087;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 40S ribosomal protein S30.

GN (RPS30A OR YLR287BC OR L8003.23) AND (RPS30B OR YOR182C).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE (RPS30A).
 RC STRAIN=YR141;
 RX MEDLINE=96278780; PubMed=8662789;
 RA Baker R.T., Williamson N.A., Wettenhall R.E.H.;
 RT "The yeast homolog of mammalian ribosomal protein S30 is expressed
 RT from a duplicated gene without a ubiquitin-like protein fusion
 RT sequence. Evolutionary implications."
 RL J. Biol. Chem. 271:13549-13555(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (RPS30A).
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
 RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
 RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
 RA Miller A., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
 RA Taich A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
 RA Wilson R., Waterston R.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (RPS30B).
 RA Hughes B., Pohl T.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- MASS SPECTROMETRY: MW=6987; MW ERR=3.4; METHOD=VALDI.
 CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR S30 IN YEAST.
 CC -1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL: U48700; AAC49317.1; -;
 DR EMBL: U48699; AAC49316.1; -;
 DR EMBL: U83406; AAB41050.1; -;
 DR EMBL: U83407; AAB41051.1; -;
 DR EMBL: U17243; AAB67333.1; -;
 DR EMBL: Z75090; CAA93391.1; -;
 DR SGD: S0004278; RPS30A.
 DR SGD: S0005708; RPS30B.
 KM Ribosomal protein; Multigene family.
 FT INIT_MET 0
 SQ SEQUENCE 62 AA; 6987 MW; 65EADAED8DFC586 CRC64;
 QY 1 KVHGSIRAGKV 12
 DB 2 KVHGSIRAGKV 13
 RESULT 7
 RS30_ONCMY STANDARD; PRT; 11 AA.
 ID RS30_ONCMY
 AC P83328;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 40S ribosomal protein S30 (Fragment).
 GN FAU.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Skin mucus;
 RA Fernandes J.M.O., Smith V.J.;
 RT "A novel antimicrobial function for a ribosomal peptide from skin
 secretions of rainbow trout."
 RL Submitted (APR-2002) to the SWISS-PROT data bank.
 CC -1- FUNCTION: Has antibacterial activity against Gram-positive
 bacteria.
 CC -1- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
 KW Ribosomal protein; Antibiotic.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;
 Query Match 18.6%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KVGSLARAGK 11
 DB 1 KVGSLARAGK 11
 RESULT 8
 HNS_PROVU STANDARD; PRT; 133 AA.
 AC P18818;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE DNA-binding protein H-NS (Histone-like protein HLP-II).
 GN HNS OR HNSA.
 OS Proteus vulgaris.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Proteus.
 OX NCBI_TaxID=585;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89171270; PubMed=2494066;
 RA Teana A., Falconi M., Scariato V., Lammi M., Pon C.L.;
 RT "Characterization of the structural genes for the DNA-binding protein
 H-NS in Enterobacteriaceae."
 RL FEBS Lett. 244:34-38(1989).
 CC -1- FUNCTION: H-NS BINDS TIGHTLY TO DS-DNA, INCREASES ITS THERMAL
 STABILITY AND INHIBITS TRANSCRIPTION. IT ALSO BINDS TO SS-DNA AND
 RNA BUT WITH A MUCH LOWER AFFINITY. H-NS HAS POSSIBLE HISTONE-LIKE
 FUNCTION. MAY BE A GLOBAL TRANSCRIPTIONAL REGULATOR THROUGH ITS
 ABILITY TO BIND TO CURVED DNA SEQUENCES, WHICH ARE FOUND IN
 REGIONS UPSTREAM OF A CERTAIN SUBSET OF PROMOTERS. IT PLAYS A ROLE
 IN THE THERMAL CONTROL OF PILI PRODUCTION. IT IS SUBJECT TO
 TRANSCRIPTIONAL AUTO-REPRESSION. IT BINDS PREFERENTIALLY TO THE
 UPSTREAM REGION OF ITS OWN GENE RECOGNIZING TWO SEGMENTS OF DNA ON
 BOTH SIDES OF A BEND CENTERED AROUND -150 (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE-LIKE PROTEIN H-NS FAMILY.
 DR PIR: S02776; S02776.
 DR HSP: P08936; 1HNR.
 DR InterPro: IPR001801; Histone_HNS.
 DR Pfam: PF00816; Histone_HNS; 1.
 DR ProDom: PD007337; Histone_HNS; 1.
 DR SMART: SM00528; HNS; 1.
 KW DNA-binding; Transcription regulation; Repressor.
 FT INT_MET 0
 SQ SEQUENCE 133 AA; 15134 MW; B92C49F7995C5ED5 CRC64;
 Query Match 11.9%; Score 7; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 28 KTGRAKR 34

DB 82 KTGRAKR 88
 RESULT 9
 YQC2_CAEEL STANDARD; PRT; 346 AA.
 ID YQC2_CAEEL
 AC Q09261;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 39.2 kDa protein C32A3.2 in chromosome III.
 GN C32A3.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Thomas K.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 CC EMBL: Z48241; CAA88285.1; -.
 DR WormPep: C32A3.2; CE01506.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 346 AA; 39221 MW; D511225F5062B420 CRC64;
 Query Match 11.9%; Score 7; DB 1; Length 346;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 23 EKKKKK 29
 DB 6 EKKKKK 12
 RESULT 10
 COLB_HUMAN STANDARD; PRT; 489 AA.
 ID COLB_HUMAN
 AC Q9BR76;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coronin 1B (Coronin 2).
 GN CORO1B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Placenta;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY BE INVOLVED IN CYTOKINESIS, MOTILITY, AND SIGNAL
 TRANSDUCTION (BY SIMILARITY).
 CC -1- SUBUNIT: BINDS ACTIN (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
 CC -----
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DR EMBL; BC006449; AAH06449.1; -
 DR Genew; HGNC:2253; CORO1B.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 3.
 DR ProDom; PD000018; WD40; 1.
 DR SMART; SM003320; WD40; 3.
 DR PROSITE; PS00678; WD_REPEATS_1; 1.
 DR PROSITE; PS00082; WD_REPEATS_2; 2.
 DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
 KW Actin-binding; Repeat; WD repeat; Coiled coil.
 FT REPEAT 80 120 WD 1.
 FT REPEAT 130 170 WD 2.
 FT REPEAT 174 213 WD 3.
 FT REPEAT 217 260 WD 4.
 FT REPEAT 265 305 WD 5.
 FT DOMAIN 449 474 COILED COIL (POTENTIAL).
 SQ SEQUENCE 489 AA; 54234 MW; A6012FDA683ECB59 CRC64;

Query Match 11.9%; Score 7; DB 1; Length 489;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSLARAG 10

|||||

Db 442 GSLARAG 448

RESULT 11

POLS_EEVVM
 ID POLS_EEVVM STANDARD; PRT; 1254 AA.
 AC P26331; Q66587; Q66588; Q66589; Q66590; Q66591;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Structural polyprotein (p130) [Contains: Coat protein C (EC 3.4.21.-)
 (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
 6 kDa peptide; Spike glycoprotein E1].
 DE Venezuelan equine encephalitis virus (strain Mena II).
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 OX NCBI_TaxID=36384;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93187617; PubMed=8445371;
 RA Snider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.;
 RT "Molecular evidence that epizootic Venezuelan equine encephalitis
 (VEE) I-AB viruses are not evolutionary derivatives of enzootic VEE
 subtype I-E or II viruses."
 RT J. Gen. Virol. 74:519-523 (1993).
 RL J. Gen. Virol. 74:519-523 (1993).
 CC -!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
 CC -!- PTM: SPECIFIC ENZYMIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 CC -!- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL
 CC SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
 CC HEMAGGLUTININ.
 CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
 CC
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DR EMBL; L04599; AAA42990.1; -
 DR EMBL; L04599; AAA42989.1; ALT_TERM.
 DR EMBL; L04599; AAA42991.1; ALT_SEQ.
 DR EMBL; L04599; AAA42992.1; ALT_SEQ.
 DR EMBL; L04599; AAA42993.1; ALT_SEQ.

DR EMBL; L04599; AAA42994.1; ALT_INIT.
 DR PIR; JQ1979; JQ1979.
 DR HSSP; P03315; IVCP.
 DR MEROPS; S03.001; -
 DR InterPro; IPR002548; Alpha_E1_glycop.
 DR InterPro; IPR000936; Alpha_E2_glycop.
 DR InterPro; IPR002533; Alpha_E3_glycop.
 DR InterPro; IPR001836; Alpha_core.
 DR InterPro; IPR000930; Togavirin.
 DR Pfam; PF00943; Alpha_E2_glycop; 1.
 DR Pfam; PF00944; Alpha_core; 1.
 DR Pfam; PF01563; Alpha_E3_glycop; 1.
 DR Pfam; PF01589; Alpha_E1_glycop; 1.
 DR PRINTS; PR00798; TOGAVIRIN.
 KW Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
 Serine protease.
 FT CHAIN 1 274 COAT PROTEIN C.
 FT CHAIN 275 333 SPIKE GLYCOPROTEIN E3.
 FT CHAIN 334 756 SPIKE GLYCOPROTEIN E2.
 FT CHAIN 757 812 6 KDA PEPTIDE.
 FT CHAIN 813 1254 SPIKE GLYCOPROTEIN E1.
 FT ACT_SITE 151 151 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 157 157 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 225 225 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT TRANSMEM 701 721 POTENTIAL.
 FT TRANSMEM 794 813 POTENTIAL.
 FT TRANSMEM 1231 1248 POTENTIAL.
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 946 946 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1254 AA; 138343 MW; FB9DE88265F20211 CRC64;

Query Match 11.9%; Score 7; DB 1; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 22;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30

|||||

Db 88 KKKKKTG 94

RESULT 12

R27A_DICDI
 ID R27A_DICDI STANDARD; PRT; 78 AA.
 AC P14797;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE 40S ribosomal protein S27a.
 OS Dictyostellium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostellium.
 OX NCBI_TaxID=44889;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352609; PubMed=2548604;
 RA Ohmachi T., Giorda R., Shaw D.R., Ennis H.L.;
 RT "Molecular organization of developmentally regulated Dictyostellium
 discoideum ubiquitin cDNAs";
 RL Biochemistry 28:5226-5231 (1989).
 CC -!- MISCELLANEOUS: THIS RIBOSOMAL PROTEIN IS SYNTHESIZED AS A
 CC C-TERMINAL EXTENSION PROTEIN (CEP) OF UBIQUITIN.
 CC -!- SIMILARITY: BELONGS TO THE S27AE FAMILY OF RIBOSOMAL PROTEINS.
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DR EMBL; M23750; AAA33264.1; ALT_INIT.
DR PIR; E34080; UQDOR7.
DR DictVdb; D001026; .
DR InterPro; IPR002906; Ribosomal_S27.
DR Pfam; PF01599; Ribosomal_S27; 1.
KW Ribosomal protein; Zinc-finger; Metal-binding.
FT DOMAIN 1 24 LYS-RICH (HIGHLY BASIC).
FT ZN_FING 46 69 C4-TYPE.
SQ SEQUENCE 78 AA; 8915 MW; F77B3E09D1B7246F CRC64;

Query Match 10.2%; Score 6; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKT 29
DB 4 KKKKKT 9

RESULT 13
RS18_BACSU
ID RS18_BACSU STANDARD; PRT; 78 AA.
AC P21475;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S18 (BS21).
GN RPSR.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051395; PubMed=7584024;
RA Ogawara N., Nakai S., Yoshikawa H.;
RA "Systematic sequencing of the 180 kilobase region of the Bacillus
RT subtilis chromosome containing the replication origin."
RL DNA Res. 1:1-14(1994).
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."

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RL Nature 390:249-256(1997).
RN 13;
RP SEQUENCE OF 1-23.
RX MEDLINE=82219212; PubMed=6806564;
RA Higo K.I., Otake E., Osawa S.;
RT "Purification and characterization of 30S ribosomal proteins from
RT Bacillus subtilis: correlation to Escherichia coli 30S proteins."
RL Mol. Gen. Genet. 185:239-244(1982).
CC 1- FUNCTION: This protein has been implicated in aminoacyl-transfer
CC RNA binding. It appears to be situated at the decoding site of
CC messenger RNA.
CC 1- SIMILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL PROTEINS.
CC 1- SIMILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL PROTEINS.
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CC
CC EMBL; D26185; BAA05219.1; ALT_INIT.
CC EMBL; 299124; CAB16126.1; ALT_INIT.
CC PIR; S11368; S11368.
CC Subtilist; BG10047; rpsr.
CC InterPro; IPR001648; Ribosomal_S18.
CC Pfam; PF01084; Ribosomal_S18; 1.
CC PRINTS; PR00974; RIBOSOMALS18.
CC ProDom; PD002239; Ribosomal_S18; 1.
CC TIGRFAMS; TIGR00165; S18; 1.
CC PROSITE; PS00057; RIBOSOMAL_S18; 1.
KW Ribosomal protein; RNA-binding; Complete proteome.
FT INIT_MET 0
SQ SEQUENCE 78 AA; 8838 MW; 1CF19CE039C64FF2 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GRAKRR 35
DB 7 GRAKRR 12

RESULT 14
EX7S_VIBCH STANDARD; PRT; 80 AA.
ID EX7S_VIBCH STANDARD; PRT; 80 AA.
AC Q9KTL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable exodeoxyribonuclease VII small subunit (EC 3.1.11.6)
DE (Exonuclease VII small subunit).
GN XSEB OR VC0891.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN 11;
RP SEQUENCE FROM N.A.
RX STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
CC 1- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INTO LARGE
CC ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURTHER
CC

```

```
CC INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
CC -|- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
CC or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
CC -|- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS (BY
CC SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: BELONGS TO THE XSEB FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE004173; AAF94053.1; -.
DR TIGR: VC0891; -.
DR InterPro: IPR003761; Exonuc_VII_S.
DR Pfam: PF02609; Exonuc_VII_S; 1.
DR TIGRFAMs: TIGR01280; xseB; 1.
KW Hydrolase; Nuclease; Exonuclease; Complete proteome.
SQ SEQUENCE 80 AA; 8911 MW; F9B7F5A9C6821BD1 CRC64;
-----
Query Match 10.2%; Score 6; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SLARAG 10
DB 44 SLARAG 49
-----
RESULT 15
YGRM_MICEC
ID YGRM_MICEC STANDARD; PRT; 105 AA.
AC P24620;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in grm 3' region (Fragment).
OS Micromonospora echinospora (Micromonospora purpurea).
CC Bacteria; Actinobacteria; Actinobacteridae; Actinobacteridae;
CC Actinomycetales; Micromonosporineae; Micromonosporaceae;
CC Micromonospora.
CC NCBI_TaxID=1877;
CC [1]
CC SEQUENCE FROM N.A.
RX MEDLINE=91192615; PubMed=2013410;
RA Kelemen G.H., Cundliffe E., Financsek I.;
RT "Cloning and characterization of gentamicin-resistance genes from
RT Micromonospora purpurea and Micromonospora rosea.";
RL Gene 98:53-60(1991).
-----
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CC -----
DR EMBL: M55520; AAA25337.1; -.
DR PIR: PW0017; PW0018.
KW Antibiotic resistance; Hypothetical protein.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11111 MW; 0B398039381DB012 CRC64;
-----
Query Match 10.2%; Score 6; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SLARAG 10
DB 44 SLARAG 49
-----
INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
-|- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
-|- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS (BY
SIMILARITY).
-|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-|- SIMILARITY: BELONGS TO THE XSEB FAMILY.
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-----
EMBL: M55520; AAA25337.1; -.
PIR: PW0017; PW0018.
KW Antibiotic resistance; Hypothetical protein.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11111 MW; 0B398039381DB012 CRC64;
-----
Query Match 10.2%; Score 6; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SLARAG 10
DB 44 SLARAG 49
-----
```

```
Db 11 SLARAG 16
-----
RESULT 16
YGRM_MICRO
ID YGRM_MICRO STANDARD; PRT; 105 AA.
AC P24621;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in grm 3' region (Fragment).
OS Micromonospora rosea.
CC Bacteria; Actinobacteria; Actinobacteridae; Actinobacteridae;
CC Actinomycetales; Micromonosporineae; Micromonosporaceae;
CC Micromonospora.
CC NCBI_TaxID=1878;
CC [1]
CC SEQUENCE FROM N.A.
RX MEDLINE=91192615; PubMed=2013410;
RA Kelemen G.H., Cundliffe E., Financsek I.;
RT "Cloning and characterization of gentamicin-resistance genes from
RT Micromonospora purpurea and Micromonospora rosea.";
RL Gene 98:53-60(1991).
-----
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CC -----
DR EMBL: M55521; AAA25339.1; -.
DR PIR: PW0018; PW0018.
KW Antibiotic resistance; Hypothetical protein.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11112 MW; 56125793440BA48C CRC64;
-----
Query Match 10.2%; Score 6; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SLARAG 10
DB 11 SLARAG 16
-----
RESULT 17
RL19_TREPA
ID RL19_TREPA STANDARD; PRT; 123 AA.
AC O83879;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 50S ribosomal protein L19.
GN RPLS OR rp0909.
OS Treponema pallidum.
CC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
CC NCBI_TaxID=160;
CC [1]
CC SEQUENCE FROM N.A.
RX STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
```

RL Science 281:375-388(1998).
 CC -1- FUNCTION: THIS PROTEIN IS LOCATED AT THE 30S-50S RIBOSOMAL SUBUNIT
 CC INTERFACE AND MAY PLAY A ROLE IN THE STRUCTURE AND FUNCTION OF THE
 CC AMINOACYL-TRNA BINDING SITE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL; AE001259; AAC65861.1; -
 CC TRER; TP0909; -
 CC InterPro: IPR001857; Ribosomal_L19.
 CC Pfam; PF01245; Ribosomal_L19; 1.
 CC PRINTS; PR00061; Ribosomal_L19.
 CC ProDom; PD002979; Ribosomal_L19; 1.
 CC TIGRFAMs; TIGR01024; rPLS.bact; 1.
 CC PROSITE; PS01015; RIBOSOMAL_L19; 1.
 CC Ribosomal protein; Complete proteome.
 CC KW RIBOSOMAL PROTEIN; COMPLETE PROTEOME.
 CC SEQUENCE 123 AA; 14192 MW; 123E652CB4B545EF CRC64;
 CC -----
 CC Query Match 10.2%; Score 6; DB 1; Length 123;
 CC Best Local Similarity 100.0%; Pred. No. 32;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 8 RAGKVR 13
 CC DB 89 RAGKVR 94
 CC | | | | |
 CC -----
 CC RESULT 18
 CC RS25_HUMAN STANDARD; PRT; 125 AA.
 CC AC P25111;
 CC DT 01-MAY-1992 (Rel. 22, Created)
 CC DT 01-MAY-1992 (Rel. 22, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE 40S ribosomal protein S25.
 CC GN RPS25.
 CC OS Homo sapiens (Human),
 CC OS Mus musculus (Mouse), and
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606, 10090, 10116;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=Human;
 CC RA MEDLINE=92084127; PubMed=17483303;
 CC RX Li M., Latoud C., Center M.S.;
 CC RT "Cloning and sequencing a cDNA encoding human ribosomal protein S25";
 CC RL Gene 107:329-333(1991).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=Human;
 CC RX MEDLINE=21864036; PubMed=11875025;
 CC RY Yoshihama M., Uechi T., Asakawa S., Kawasaki K., Kato S., Higa S.,
 CC Maeda N., Minoshima S., Tanaka T., Shimizu N., Kenmochi N.;
 CC RT "The human ribosomal protein genes: sequencing and comparative
 CC analysis of 73 genes";
 CC RL Genome Res. 12:379-390(2002).
 CC RN [3]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=Human;
 CC RX Strausberg R.;
 CC RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC RN [4]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=Mouse; STRAIN=C57BL/6J;
 CC -----

RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Harai A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection";
 RA Nature 409:685-690(2001).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP SPECIES=Mouse; TISSUE=Breast tumor;
 RC Strausberg R.;
 RN Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Rat; STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=92378645; PubMed=1354961;
 RA Chan Y.-L., Wool I.G.;
 RT "The primary structure of rat ribosomal protein S25";
 RL Biochem. Biophys. Res. Commun. 186:1688-1693(1992).
 CC -1- SIMILARITY: BELONGS TO THE S25E FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 CC EMBL; M64716; AAA16105.1; -
 CC EMBL; AB061844; BAB79482.1; -
 CC EMBL; BC003537; AAH03537.1; -
 CC EMBL; BC004294; AAH04294.1; -
 CC EMBL; BC004986; AAH04986.1; -
 CC EMBL; AK012696; BAB28417.1; -
 CC EMBL; BC002088; AAH02088.1; -
 CC EMBL; X62482; CAA44349.1; -
 CC PIR; S17353; R3RT25.
 CC PIR; JH0691; JH0691.
 CC PIR; JQ1347; JQ1347.
 CC Genew; HGNC:10413; RPS25.
 CC MIM; 180465; -
 CC MGD; MGI:1922867; Rps25.
 CC InterPro; IPR004977; Ribosomal_S25.
 CC Pfam; PF03297; Ribosomal_S25; 1.
 CC KW Ribosomal protein.
 CC SEQUENCE 125 AA; 13742 MW; B8E05F04FCF2F1A9 CRC64;
 CC -----
 CC Query Match 10.2%; Score 6; DB 1; Length 125;
 CC Best Local Similarity 100.0%; Pred. No. 33;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 4 GSLARA 9
 CC DB 81 GSLARA 86
 CC | | | | |
 CC -----
 CC RESULT 19
 CC RS11_RICPR

```

ID RS11_RICPR STANDARD; PRT; 127 AA.
AC Q9ZCS8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30S ribosomal protein S11.
GN RPSK OR RP636.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomrodipour A., Andersson J.O.,
RA Slicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC (-) FUNCTION: S11 PLAYS AN ESSENTIAL ROLE FOR THE SELECTION OF THE
CC CORRECT TRNA IN PROTEIN BIOSYNTHESIS. IT IS LOCATED ON THE LARGE
CC LOBE OF THE SMALL SUBUNIT (BY SIMILARITY).
CC (-) SIMILARITY: BELONGS TO THE S11P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
CC EMBL; AJ235272; CAAL5076.1; -
CC InterPro: IPR001971; Ribosomal_S11.
CC Pfam: PF00411; Ribosomal_S11; 1.
CC ProDom: PD001010; Ribosomal_S11; 1.
CC PROSITE; PS00054; RIBOSOMAL_S11; FALSE_NEG.
CC Ribosomal protein; Complete proteome.
CC SEQUENCE 127 AA; 13583 MW; BED96964C891616C CRC64;

Query Match 10.2%; Score 6; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKT 29
Db 8 KKKKKT 13

RESULT 20
Y082_CAEEL STANDARD; PRT; 128 AA.
ID Y082_CAEEL
AC Q09237;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 13.7 kDa protein C18H9.2 in chromosome II.
GN C18H9.2
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Faveille T.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL; U23147; AAC46687.1; -
CC WormPep; C18H9.2; CE01802.
KW Hypothetical protein.
SQ SEQUENCE 128 AA; 13666 MW; C7A64D960B95E2EC CRC64;

Query Match 10.2%; Score 6; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKT 29
Db 84 KKKKKT 89

RESULT 21
YNO3_YEAST STANDARD; PRT; 130 AA.
ID YNO3_YEAST
AC P53908;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 15.3 kDa protein in MPA2-MEP2 intergenic region.
GN YNL143C OR N1206 OR N1795.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=96109932; PubMed=8619318;
RA Mallet L., Bussereau F., Jacquet M.;
RT "A 43.5 kb segment of yeast chromosome XIV, which contains MPA2,
RT MEP2, CAP/SRV2, NAM9, FKBI/PPRI/RBP1, MOM22 and CPT1, predicts an
RT adenosine deaminase gene and 14 new open reading frames.";
RL Yeast 11:1195-1209(1995).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; 246843; CAA86883.1; -
CC EMBL; 271419; CAA96026.1; -
CC SGD; S0005087; YNL143C.
KW Hypothetical protein.
SQ SEQUENCE 130 AA; 15319 MW; 29070E47FC63436D CRC64;

Query Match 10.2%; Score 6; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
Db 48 EKKKKK 53

RESULT 22
YKDL_YEAST STANDARD; PRT; 137 AA.
ID YKDL_YEAST
AC P36098;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 15.6 kDa protein in IXR1-TRAI intergenic region.

```

GN YKL031W OR YKL244.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94262309; PubMed=8203146;
RA Purnelle B., Skala J., van Dyck L., Goffeau A.;
RT "Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new
RT tRNA gene and four new open reading frames including a leucine zipper
RL protein and a homologue to the yeast mitochondrial regulator ABF2.";
RN Yeast 10:125-130(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Rieger M.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL; X71622; NOT_ANNOTATED_CDS.
DR EMBL; Z28031; CAA81866.1; -.
DR PIR; S37848;
DR SGD; S0001514; YKL031W.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 36 52 POTENTIAL.
FT TRANSMEM 113 129 POTENTIAL.
SQ SEQUENCE 137 AA; 15626 MW; 82908E55C7E37CFC CRC64;

Query Match 10.2%; Score 6; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
DB 60 EKKKKK 65

RESULT 23
RS16_CANAL STANDARD; PRT; 142 AA.
AC Q94017;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 40S ribosomal protein S16.
GN RPS16 OR CA49C10.OIC.
OC Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1161;
RA Taylor K., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -----
CC -!- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----

DR EMBL; AL033497; CAA21965.1; -.
DR InterPro; IPR000754; Ribosomal_S9.
DR Pfam; PF00380; Ribosomal_S9; 1.
DR ProDom; PD001627; Ribosomal_S9; 1.
DR PROSITE; PS00360; RIBOSOMAL_S9; 1.
KW Ribosomal protein.
SQ SEQUENCE 142 AA; 15739 MW; 19408A7791FF4356 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TFGKKK 53
DB 8 TFGKKK 13

RESULT 24
RS16_YEAST STANDARD; PRT; 142 AA.
ID RS16_YEAST
AC P40213; P26787;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 40S ribosomal protein S16 (RP61R).
GN (RPS16A OR RP61R OR YMR143W OR YMR9375.12) AND (RPS16B OR YDL083C).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A. (RPS16A).
RC STRAIN=S288C / AB972;
RA Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (RPS16B).
RA Wambutt R., Wedler H., Wedler E., Scharfe M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE OF 1-25.
RX MEDLINE=92184799; PubMed=1544921;
RA Takakura H., Tsunasawa S., Miyagi M., Warner J.R.;
RT "NH2-terminal acetylation of ribosomal proteins of Saccharomyces
RT cerevisiae";
RL J. Biol. Chem. 267:5442-5445(1992).
CC -----
CC -!- MISCELLANEOUS: THERE ARE TWO GENES FOR S16 IN YEAST.
CC -!- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL; Z47071; CAA87357.1; -.
DR EMBL; Z74131; CAA98649.1; -.
DR SGD; S0004751; RPS16A.
DR SGD; S0002241; RPS16B.
DR InterPro; IPR000754; Ribosomal_S9.
DR Pfam; PF00380; Ribosomal_S9; 1.
DR ProDom; PD001627; Ribosomal_S9; 1.
DR PROSITE; PS00360; RIBOSOMAL_S9; 1.
KW Ribosomal protein; Acetylation; Multigene family.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 142 AA; 15716 MW; 15873374B3262144 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TFGKKK 53
|||||
Db 8 TFGKKK 13

```
RESULT 25
END7_BPT4
ID END7_BPT4 STANDARD; PRT; 157 AA.
AC P13340; Q38426; Q9T0V4;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Recombination endonuclease VII (EC 3.1.1.-) (Protein Gp49).
GN 49.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10865;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C;
RX MEDLINE=87203398; PubMed=3575111;
RA Tomaszewski J., Ruger W.;
RT "Nucleotide sequence and primary structures of gene products coded
RT for by the T4 genome between map positions 48,266 kb and 39,166 kb.";
RL Nucleic Acids Res. 15:3632-3633(1987).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE INITIATION.
RX MEDLINE=89065345; PubMed=2974005;
RA Barth K.A., Powell D., Trupin M., Mosig G.;
RT "Regulation of two nested proteins from gene 49 (recombination
RT endonuclease VII) and of a lambda RexA-like protein of bacteriophage
RT T4.";
RL Genetics 120:329-343(1988).
RN [3]
RP SEQUENCE FROM N.A.
RA Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,
RA Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;
RT "Bacteriophage T4 genome analysis.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CLEAVES DNA CRUCIFORM AND Y-STRUCTURES AS WELL AS
CC HETERODUPLEX LOOPS.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms are produced by alternative
CC initiation.
CC -----
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CC -----
CC EMBL; X12629; CAA311148.1; -.
CC EMBL; X12629; CAA311149.1; -.
CC EMBL; Y00122; CAA68307.1; -.
CC EMBL; AF158101; AAD42477.1; -.
CC EMBL; AF158101; AAD42687.1; ALT_INIT.
CC PIR; A30291; ZNBPT9.
CC InterPro; IPR004211; Endonuclease_7.
CC Pfam; PF02945; endonuclease_7; 3.
KW Hydrolase; Endonuclease; Nuclease; Alternative initiation.
FT CHAIN 1 157 RECOMBINATION ENDONUCLEASE VII, LONG
FT ISOFORM.
FT CHAIN 53 157 RECOMBINATION ENDONUCLEASE VII, SHORT
FT ISOFORM.
FT INIT_MET 53 53 FOR SHORT ISOFORM.
SQ SEQUENCE 157 AA; 18144 MW; 86233D2A7FC0F9A8 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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-----
EMBL; X12629; CAA311148.1; -.
EMBL; X12629; CAA311149.1; -.
EMBL; Y00122; CAA68307.1; -.
EMBL; AF158101; AAD42477.1; -.
EMBL; AF158101; AAD42687.1; ALT_INIT.
PIR; A30291; ZNBPT9.
InterPro; IPR004211; Endonuclease_7.
Pfam; PF02945; endonuclease_7; 3.
KW Hydrolase; Endonuclease; Nuclease; Alternative initiation.
FT CHAIN 1 157 RECOMBINATION ENDONUCLEASE VII, LONG
FT ISOFORM.
FT CHAIN 53 157 RECOMBINATION ENDONUCLEASE VII, SHORT
FT ISOFORM.
FT INIT_MET 53 53 FOR SHORT ISOFORM.
SQ SEQUENCE 157 AA; 18144 MW; 86233D2A7FC0F9A8 CRC64;
```

```
QY 9 AGKVRG 14
|||||
Db 50 AGKVRG 55

RESULT 26
YK20_YEAST
ID YK20_YEAST STANDARD; PRT; 167 AA.
AC P36133;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical 19.2 kDa protein in GAPI-NAP1 intergenic region.
GN YKR040C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Urrestarazu L.A., Jauniaux J.-C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; Z28265; CAA82114.1; -.
CC EMBL; Z28266; CAA82117.1; -.
CC PIR; S38112; S38112.
CC SGD; S0001748; YKR040C.
KW Hypothetical protein.
FT DOMAIN 144 167 LYS-RICH (HIGHLY BASIC).
SQ SEQUENCE 167 AA; 19222 MW; 51BC98B657A720C2 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

-----
QY 23 EKKKKK 28
|||||
Db 143 EKKKKK 148

RESULT 27
RL14_LEIDO
ID RL14_LEIDO STANDARD; PRT; 175 AA.
AC Q25278;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Probable 40S ribosomal protein L14 (23 kDa cell surface protein)
DE (LDP 23).
GN RPL14 OR LDP23.
OS Leishmania donovani.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LS;
RX MEDLINE=96042140; PubMed=7595213;
RA Campos-Neto A., Soong L., Cordova J.L., Sant'Angelo D., Skeiky Y.A.W.,
RA Rudde N.H., Reed S.G., Janeway C. Jr., McMahon-Pratt D.;
RT "Cloning and expression of a Leishmania donovani gene instructed by a
RT peptide isolated from major histocompatibility complex class II
RT molecules of infected macrophages.";
RL J. Exp. Med. 182:1423-1433(1995).
CC -!- SIMILARITY: BELONGS TO THE L14E FAMILY OF RIBOSOMAL PROTEINS.
```

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 DR EMBL; X86551; CAA60246.1; -
 DR InterPro: IPR000302; KOW_motif.
 DR InterPro: IPR002784; Ribosomal_L14e.
 DR Pfam; PF00467; KOW; 1.
 DR Pfam; PF01929; Ribosomal_L14e; 1.
 KW Ribosomal protein.
 SQ SEQUENCE 175 AA; 19887 MW; A3F9AFF30D986814 CRC64;

 Query Match 10.2%; Score 6; DB 1; Length 175;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 32 AKRRMQ 37
 DB 160 AKRRMQ 165
 |||||

 RESULT 28
 FXV5_MOUSE
 ID FXV5_MOUSE STANDARD; PRT; 178 AA.
 AC P97808;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE FXV5 domain-containing ion transport regulator 5 precursor
 DE (Oncoprotein-induced protein 2) (Ion channel homolog RIC) (EP-8).
 GN FXV5 OR OIT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=97184476; PubMed=9032278;
 RA Fu X., Kamps M.P.;
 RT "p2a-phx1 induces aberrant expression of tissue-specific and
 RT developmentally regulated genes when expressed in NIH 3T3
 RT fibroblasts.";
 RL Mol. Cell. Biol. 17:1503-1512(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spleen;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schriml L.M., StaUBL F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).

 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: SPLEEN, LUNG, SKELETAL MUSCLE, AND TESTIS.
 CC -!- DEVELOPMENTAL STAGE: EXHIBITS BIPHASIC EXPRESSION DURING
 CC DEVELOPMENT.
 CC -!- SIMILARITY: BELONGS TO THE FXVD FAMILY.

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 DR EMBL; U72680; AAB51040.1; -
 DR EMBL; AK003068; BAB22545.1; -
 DR MGD; MGI:1201785; Fxyd5.
 DR InterPro: IPR000272; ATP1G1_PLM_MAT8.
 DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
 DR PROSITE; PS01310; FXYD; 1.
 KW Transmembrane; Signal; Ionic channel; Ion transport.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 178 FXYD DOMAIN-CONTAINING ION TRANSPORT
 FT REGULATOR 5.
 FT DOMAIN 22 145 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 146 166 POTENTIAL.
 FT DOMAIN 167 178 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 88 134 PRO-RICH.
 SQ SEQUENCE 178 AA; 19454 MW; 466FBF1E05D861C5 CRC64;

 Query Match 10.2%; Score 6; DB 1; Length 178;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 13 RGQTPK 18
 DB 20 RGQTPK 25
 |||||

 RESULT 29
 CC42_CAEL
 ID CC42_CAEL STANDARD; PRT; 188 AA.
 AC Q05062;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cell division control protein 42 homolog (CDC42CE).
 GN CDC-42 OR R07G3.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=93293845; PubMed=8514766;
 RA Chen W., Lim H., Lim L.;
 RA "The CDC42 homologue from Caenorhabditis elegans. Complementation of
 RT yeast mutation.";
 RL J. Biol. Chem. 268:13280-13285(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS AT THE EMBRYONIC STAGE,
 CC DECREASING PROGRESSIVELY DURING DEVELOPMENT, EXCEPT FOR AN
 CC INCREASE AT THE L3 STAGE.
 CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
 CC CDC42 SUBFAMILY.

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CC EMBL; LI0078; AAA51433.1; .
 CC EMBL; U23452; AAK31543.1; ALT_INIT.
 CC PIR; A46578; A46578.
 CC HSSP; P21181; 1AM4.
 CC WormPep; R07G3.1; CE02020.
 CC InterPro; IPR003578; GTPase_Rho.
 CC InterPro; IPR001806; Ras trnsfrmng.
 CC InterPro; IPR005225; Small_GTP.
 CC Pfam; PF00071; ras; 1.
 CC PRINTS; PR00449; RASTRNSFRMNG.
 CC SMART; SM00174; RHO; 1.
 CC TIGRFAMS; TIGR00231; small_GTP; 1.
 CC GTP-binding; Lipoprotein; Cell cycle; Cell division; Prenylation.
 CC FT NP_BIND 7 14 GTP (BY SIMILARITY).
 CC FT NP_BIND 54 58 GTP (BY SIMILARITY).
 CC FT NP_BIND 112 115 GTP (BY SIMILARITY).
 CC FT DOMAIN 29 37 EFFECTOR REGION (BY SIMILARITY).
 CC FT LIPID 185 185 GERANYL-GERANYL (BY SIMILARITY).
 CC SEQUENCE 188 AA; 20823 MW; 873395896B681299 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 188;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QEKKKK 27
 |||||
 DB 179 QEKKKK 184

RESULT 30
 RASK_MELGA
 ID RASK_MELGA STANDARD; PRT; 188 AA.
 AC P79800;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Transforming protein p21 (K-Ras) (K1-Ras).
 GN KRAS.
 OS Meleagris gallopavo (Common turkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 CC NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Spleen;
 RX MEDLINE=97080492; PubMed=6921837;
 RA Chajut A., Gazit A., Yaniv A.;
 RT "The turkey c-rapLA proto-oncogene is expressed via two distinct
 RT promoters.";
 RL Gene 177:7-10(1996).
 CC -1- FUNCTION: RAS PROTEINS BIND GDP/GTP AND POSSESS INTRINSIC GTPASE
 CC ACTIVITY.
 CC -1- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
 CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE
 CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
 CC ACTIVATING PROTEIN (GAP).
 CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
 CC -----
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CC EMBL; X85754; CAA59755.1; .

DR HSSP; P01112; 1PLL.
 DR InterPro; IPR003577; GTPase_Ras.
 DR InterPro; IPR001230; Prenyl_site.
 DR InterPro; IPR001806; Ras trnsfrmng.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF00071; ras; 1.
 DR PRINTS; PR00449; RASTRNSFRMNG.
 DR SMART; SM00173; RAS; 1.
 DR TIGRFAMS; TIGR00231; small_GTP; 1.
 CC GTP-binding; Lipoprotein; Cell cycle; Cell division; Prenylation.
 CC FT NP_BIND 10 17 GTP (BY SIMILARITY).
 CC FT NP_BIND 57 61 GTP (BY SIMILARITY).
 CC FT NP_BIND 116 119 GTP (BY SIMILARITY).
 CC FT DOMAIN 32 40 EFFECTOR REGION (BY SIMILARITY).
 CC FT LIPID 185 185 FARNESYL (BY SIMILARITY).
 CC SEQUENCE 188 AA; 21452 MW; AAB6C319BB259865 CRC64;
 Query Match 10.2%; Score 6; DB 1; Length 188;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKT 29
 |||||
 DB 176 KKKKKT 181

RESULT 31
 PAPH_ECOLI
 ID PAPH_ECOLI STANDARD; PRT; 195 AA.
 AC P07111;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PAP fimbrial minor pilin protein precursor.
 GN PAPH.
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 CC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-J96;
 RX MEDLINE=87187619; PubMed=2882856;
 RA Baga M., Norgren M., Normark S.;
 RT "Biogenesis of E. coli Pap pili: paph, a minor pilin subunit involved
 RT in cell anchoring and length modulation.";
 RL Cell 49:241-251(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-J96;
 RX MEDLINE=93023852; PubMed=1357526;
 RA Marklund B.-I., Tennent J.M., Garcia E., Hamers A., Baga M.,
 RA Lindberg F., Gastra W., Normark S.;
 RT "Horizontal gene transfer of the Escherichia coli pap and prs pili
 RT operons as a mechanism for the development of tissue-specific
 RT adhesive properties.";
 RL Mol. Microbiol. 6:2225-2242(1992).
 RN [3]
 RP SEQUENCE OF 149-195 FROM N.A.
 RC STRAIN-J96;
 RX MEDLINE=89216160; PubMed=2897064;
 RA Norgren M., Baga M., Tennent J.M., Normark S.;
 RT "Nucleotide sequence, regulation and functional analysis of the papC
 RT gene required for cell surface localization of Pap pili of
 RT uropathogenic Escherichia coli.";
 RL Mol. Microbiol. 1:169-178(1987).
 CC -1- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
 CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
 CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
 CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
 CC -1- FUNCTION: PAPH SEEMS TO ANCHOR THE PILUS TO THE BACTERIAL CELL.
 CC IN ADDITION THE STOICHIOMETRIC RELATIONSHIP BETWEEN PAPH AND
 CC PAPA DETERMINES THE PILUS LENGTH.

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (39)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (40)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1633

Query Match 10.2%: Score 6; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 EKKKKK 28
Db 1 EKKKKK 6

RESULT 21
US-09-764-869-926
Sequence 926, Application US/09764869
Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 926
LENGTH: 45
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-869-926

Query Match 10.2%: Score 6; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 EKKKKK 28
Db 33 EKKKKK 38

RESULT 22
US-09-925-299-1098
Sequence 1098, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1098
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-1098

Query Match 10.2%: Score 6; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 KKKKKK 29

Db 7 KKKKKK 12

RESULT 23
US-09-983-802-479
Sequence 479, Application US/09983802
Publication No. US20030022185A1
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/983,802
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/2227,357
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954

```
RESULT 17
US-09-764-877-1043
; Sequence 1043, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1043
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1043
```

```
Query Match          10.2%: Score 6; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 23 EKKKKK 28
    |||||
Db 10 EKKKKK 15
```

```
RESULT 18
US-09-925-300-1820
; Sequence 1820, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruden,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1820
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1820
```

```
Query Match          10.2%: Score 6; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 23 EKKKKK 28
    |||||
Db 17 EKKKKK 22
```

```
RESULT 19
US-09-925-301-1640
; Sequence 1640, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (30)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1640
```

```
Query Match          10.2%: Score 6; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 23 EKKKKK 28
    |||||
Db 10 EKKKKK 15
```

```
RESULT 20
US-09-925-301-1633
; Sequence 1633, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1633
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (38)
```

```
Query Match          10.2%: Score 6; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 23 EKKKKK 28
    |||||
Db 17 EKKKKK 22
```

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (23)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (28)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1319

Query Match 10.2%; Score 6; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKK 29
|||||
DB 10 KKKKK 15

RESULT 14
US-09-071-838-189
Sequence 189, Application US/09071838
Patent No. US20020152501A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
NUMBER OF SEQUENCES: 324
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/071, 838
APPLICATION NUMBER: US/09/071, 838
FILING DATE: 01-MAY-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-086100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-071-838-189

Query Match 10.2%; Score 6; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TFGKK 53
|||||
DB 1 TFGKK 6

RESULT 15
US-09-764-846-248
Sequence 248, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P212
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 348
SOFTWARE: Patentlin Ver. 2.0
SEQ ID NO 248
LENGTH: 31
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-764-846-248

Query Match 10.2%; Score 6; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
|||||
DB 5 EKKKK 10

RESULT 16
US-09-925-299-1474
Sequence 1474, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentlin Ver. 2.0
SEQ ID NO 1474
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (25)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (30)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1474

Query Match 10.2%; Score 6; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
|||||
DB 17 EKKKK 22

```
; INFORMATION FOR SEQ ID NO: 201:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 16 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-438-486-201

Query Match
Best Local Similarity 10.2%; Score 6; DB 9; Length 16;
Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
Db 8 EKKKK 13

RESULT 11
US-09-764-869-729
; Sequence 729, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION DATA REMOVED - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 729
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-869-729

Query Match
Best Local Similarity 10.2%; Score 6; DB 10; Length 17;
Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
Db 10 EKKKK 15

RESULT 12
US-09-864-761-41097
; Sequence 41097, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
```

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41097
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013746.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL - 3.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL - 5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 2.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL - 5.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL - 5.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL - 5.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 3.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL - 4.8
US-09-864-761-41097

Query Match
Best Local Similarity 10.2%; Score 6; DB 10; Length 24;
Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
Db 6 EKKKK 11

RESULT 13
US-09-925-299-1319
; Sequence 1319, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1319
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (17)
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;; CURRENT FILING DATE: 2001-08-31
;; PRIOR APPLICATION NUMBER: 09/041,990
;; PRIOR FILING DATE: 2001-01-13
;; PRIOR APPLICATION NUMBER: 08/771,212
;; PRIOR FILING DATE: 1996-12-20
;; PRIOR APPLICATION NUMBER: 08/531,319
;; PRIOR FILING DATE: 1996-04-11
;; NUMBER OF SEQ ID NOS: 89
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 87
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Peptide that
;; OTHER INFORMATION: corresponds to the C-termini of Frase or Ggtase
;; OTHER INFORMATION: substrates
US-09-945-249-87

Query Match 10.2%; Score 6; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
Db 6 EKKKK 11

RESULT 9
US-09-843-676-201
; Sequence 201, Application US/09843676
; Patent No. US20020164786A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-May-1997

APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-Oct-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 201:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 201:
US-09-843-676-201

Query Match 10.2%; Score 6; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
Db 8 EKKKK 13

RESULT 10
US-09-438-486-201
; Sequence 201, Application US/09438486
; Publication No. US2003009019A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
TITLE OF INVENTION: No. US2003009019A1 Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-Nov-1999
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-May-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-Apr-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-Apr-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-Oct-1996
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

OY 23 EKKKKKT 29
|||||
Db 21 EKKKKKT 27

RESULT 4
US-09-764-877-1759
; Sequence 1759, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1759
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1759

Query Match 11.9%; Score 7; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKKT 29
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Db 114 EKKKKKT 120

RESULT 5
US-09-774-639-155
; Sequence 155, Application US/09774639
; Publication No. US20030003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 155
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-155

Query Match 11.9%; Score 7; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKKT 29
|||||
Db 220 EKKKKKT 226

RESULT 6
US-10-014-717-5
; Sequence 5, Application US/10014717
; Publication No. US20020192778A1
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern

; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/10/014,717
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US/09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-10-014-717-5

Query Match 11.9%; Score 7; DB 9; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAGK 11
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Db 7250 SLARAGK 7256

RESULT 7
US-09-983-067-1
; Sequence 1, Application US/09983067
; Patent No. US20020123101A1
; GENERAL INFORMATION:
; APPLICANT: INOUE, Akio
; APPLICANT: SHIMIZU, Yoshihiro
; APPLICANT: UEDA, Takuya
; TITLE OF INVENTION: Process for Producing Peptides By Using In Vitro
; TITLE OF INVENTION: Transcription/Translation System
; FILE REFERENCE: 1752-0151P
; CURRENT APPLICATION NUMBER: US/09/983,067
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: JP 294795/2001
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: JP 227094/2001
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: JP 6910/2001
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: JP 401417/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Bovine sp.
US-09-983-067-1

Query Match 10.2%; Score 6; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKK 28
|||||
Db 9 EKKKKK 14

RESULT 8
US-09-945-249-87
; Sequence 87, Application US/09945249
; Patent No. US20020168748A1
; GENERAL INFORMATION:
; APPLICANT: BERLIN, VIVIAN
; APPLICANT: DAMAGNEZ, VERONIQUE
; APPLICANT: SMITH, SUSAN E.
; TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,
; FILE REFERENCE: MIV-074_06
; CURRENT APPLICATION NUMBER: US/09/945,249

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1 APPLICANT: Hanzel, David K.
2 APPLICANT: Chen, Wensheng
3 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
4 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
5 FILE REFERENCE: Aecm1ca-x-1
6 CURRENT APPLICATION NUMBER: US/09/864,761
7 CURRENT FILING DATE: 2001-05-23
8 PRIOR APPLICATION NUMBER: US 60/180,312
9 PRIOR FILING DATE: 2000-02-04
10 PRIOR APPLICATION NUMBER: US 60/207,456
11 PRIOR FILING DATE: 2000-05-26
12 PRIOR APPLICATION NUMBER: US 09/632,366
13 PRIOR FILING DATE: 2000-08-03
14 PRIOR APPLICATION NUMBER: GB 24263.6
15 PRIOR FILING DATE: 2000-10-04
16 PRIOR APPLICATION NUMBER: US 60/236,359
17 PRIOR FILING DATE: 2000-09-27
18 PRIOR APPLICATION NUMBER: PCT/US01/00666
19 PRIOR FILING DATE: 2001-01-30
20 PRIOR APPLICATION NUMBER: PCT/US01/00667
21 PRIOR FILING DATE: 2001-01-30
22 PRIOR APPLICATION NUMBER: PCT/US01/00664
23 PRIOR FILING DATE: 2001-01-30
24 PRIOR APPLICATION NUMBER: PCT/US01/00669
25 PRIOR FILING DATE: 2001-01-30
26 PRIOR APPLICATION NUMBER: PCT/US01/00665
27 PRIOR FILING DATE: 2001-01-30
28 PRIOR APPLICATION NUMBER: PCT/US01/00668
29 PRIOR FILING DATE: 2001-01-30
30 PRIOR APPLICATION NUMBER: PCT/US01/00663
31 PRIOR FILING DATE: 2001-01-30
32 PRIOR APPLICATION NUMBER: PCT/US01/00662
33 PRIOR FILING DATE: 2001-01-30
34 PRIOR APPLICATION NUMBER: PCT/US01/00661
35 PRIOR FILING DATE: 2001-01-30
36 PRIOR APPLICATION NUMBER: PCT/US01/00670
37 PRIOR FILING DATE: 2001-01-30
38 PRIOR APPLICATION NUMBER: US 60/234,687
39 PRIOR FILING DATE: 2000-09-21
40 PRIOR APPLICATION NUMBER: US 09/608,408
41 PRIOR FILING DATE: 2000-06-30
42 PRIOR APPLICATION NUMBER: US 09/774,203
43 PRIOR FILING DATE: 2001-01-29
44 NUMBER OF SEQ ID NOS: 49117
45 SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
46 SEQ ID NO 35333
47 LENGTH: 118
48 TYPE: PRT
49 ORGANISM: Homo sapiens
50 FEATURE:
51 OTHER INFORMATION: MAP TO AC009704.2
52 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 19
53 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8
54 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 18
55 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.5
56 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.3
57 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.1
58 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 81
59 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 12
60 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 30
61 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 12
62 OTHER INFORMATION: SWISSPROT HIT: P35544, EVALUATE 4.00e-23
63 OTHER INFORMATION: EST_HUMAN HIT: BF347807.1, EVALUATE 6.00e-47
64 US-09-864-761-35333

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Best Local Similarity	100.0%	Pred. NO.	2	8e-19			
Matches	28	Conservative	0	Mismatches	0	Indels	0
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QY	1	KVHGS	LARAG	KVRGQT	PKVAQ	DEKKKK	28
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RESULT 3
US-09-864-761-39484
; Sequence 39484, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 39484
LENGTH: 62
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005598.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.7

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Query Match	11.9%	Score 7;	DB 10;	Length 62;					
Best Local Similarity	100.0%	Pred. No. 3.9;							
Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 21:31:19 : Search time 11 Seconds
(without alignments)
118.908 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59
Sequence: 1 KVHSLARAGKVRGQTPKVA.....RRFVNVVPTFGKKKGNPNS 59

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 129505 seqs, 22169297 residues

Word size : 0

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications_AA: *
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2: /cgn2_6/ptodata/2/pubpaa/PCIT_NEW_PUB pep: *
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	170	US-09-925-301-994	Sequence 994, App
2	28	47.5	118	US-09-864-761-35333	Sequence 35333, A
3	7	11.9	62	US-09-864-761-39484	Sequence 39484, A
4	7	11.9	121	US-09-764-877-1759	Sequence 1759, Ap
5	7	11.9	227	US-09-774-639-155	Sequence 155, App
6	7	11.9	7257	US-10-014-717-5	Sequence 5, Appl1
7	6	10.2	14	US-09-983-067-1	Sequence 1, Appl1
8	6	10.2	15	US-09-945-249-87	Sequence 87, Appl
9	6	10.2	16	US-09-843-676-201	Sequence 201, App
10	6	10.2	16	US-09-438-486-201	Sequence 201, App
11	6	10.2	17	US-09-764-869-729	Sequence 729, App
12	6	10.2	24	US-09-864-761-41097	Sequence 41097, A
13	6	10.2	28	US-09-925-299-1319	Sequence 1319, Ap
14	6	10.2	29	US-09-071-838-189	Sequence 189, App
15	6	10.2	31	US-09-764-846-246	Sequence 248, App
16	6	10.2	32	US-09-925-299-1474	Sequence 1474, Ap
17	6	10.2	36	US-09-764-877-1043	Sequence 1043, App
18	6	10.2	36	US-09-925-300-1820	Sequence 1820, Ap
19	6	10.2	37	US-09-925-301-1640	Sequence 1640, Ap

20	6	10.2	43	US-09-925-301-1633	Sequence 1633, Ap
21	6	10.2	45	US-09-764-869-926	Sequence 926, App
22	6	10.2	48	US-09-925-299-1098	Sequence 1098, Ap
23	6	10.2	51	US-09-983-802-479	Sequence 479, App
24	6	10.2	52	US-09-764-869-1228	Sequence 1228, Ap
25	6	10.2	55	US-09-764-855-113	Sequence 113, App
26	6	10.2	56	US-09-764-847-601	Sequence 601, App
27	6	10.2	57	US-09-864-761-47593	Sequence 47593, A
28	6	10.2	59	US-09-864-761-47812	Sequence 47812, A
29	6	10.2	60	US-09-989-919-118	Sequence 118, App
30	6	10.2	60	US-09-925-300-1198	Sequence 1198, Ap
31	6	10.2	62	US-09-925-301-1475	Sequence 1475, Ap
32	6	10.2	63	US-10-117-604-2	Sequence 2, Appl1
33	6	10.2	63	US-09-764-846-260	Sequence 260, App
34	6	10.2	64	US-09-864-761-45501	Sequence 45501, A
35	6	10.2	66	US-09-764-846-224	Sequence 224, App
36	6	10.2	67	US-09-764-877-1089	Sequence 1089, Ap
37	6	10.2	67	US-09-867-550-284	Sequence 284, App
38	6	10.2	68	US-09-201-936-18	Sequence 18, Appl
39	6	10.2	68	US-09-201-936-19	Sequence 19, Appl
40	6	10.2	68	US-09-764-846-191	Sequence 191, App
41	6	10.2	69	US-09-925-299-1340	Sequence 1340, Ap
42	6	10.2	72	US-09-764-846-179	Sequence 179, App
43	6	10.2	72	US-09-925-300-1105	Sequence 1105, Ap
44	6	10.2	73	US-09-764-846-242	Sequence 242, App
45	6	10.2	75	US-09-833-067-9	Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-09-925-301-994
Sequence 994, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925, 301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124, 270
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 994
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-994

Query Match 100.0%; Score 59; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 9.3e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHSLARAGKVRGQTPKVAOEKKKKTKGRKRMQYRRFVNVVPTFGKKKGNPNS 59
|||||
Db 112 KVHSLARAGKVRGQTPKVAOEKKKKTKGRKRMQYRRFVNVVPTFGKKKGNPNS 170

RESULT 2
US-09-864-761-35333
Sequence 35333, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.

```
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STRAINS OF E.COLI THAT CAUSE INFECTION OF THE HUMAN
CC URINARY TRACT PRODUCE PAP-PIII WHICH ARE HAIR-LIKE APPENDAGES
CC CONSISTING OF ABOUT 1000 HELICALLY ARRANGED SUBUNITS OF THE
CC PROTEIN PAPA. THESE PILI MEDIATE BINDING TO DIGALACTOSIDE-
CC CONTAINING GLYCOLIPIDS PRESENT ON THE EPITHELIAL CELLS WHICH
CC LINE THE URINARY TRACT.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
DR EMBL; Y00529; CAAB6587.1; -
DR EMBL; M16202; AAA24286.1; -
DR EMBL; X61239; CAA43563.1; -
DR PIR; A27021; YOECPH.
DR InterPro: IPR000259; Fimbrial.
DR Pfam; PF00419; Fimbrial; 1.
KW Fimbrin; Signal.
FT SIGNAL 1 22
FT CHAIN 23 195 PAP FIMBRIAL MINOR PILIN PROTEIN.
FT DISULFID 58 97 PROBABLE.
SQ SEQUENCE 195 AA; 21835 MW; D2120FCSDA063169 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ARAGV 12
DB 148 ARAGV 153

RESULT 32
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DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
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CN PRSH.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1442;
RX MEDLINE=93023852; PubMed=1357526;
RA Marklund B., Tennent J.M., Garcia E., Hamers A., Baga M.,
RA Lindberg F., Gaastra W., Normark S.;
RA "Horizontal gene transfer of the Escherichia coli pap and prs pili
RA operators as a mechanism for the development of tissue-specific
RA adhesive properties."
RL Mol. Microbiol. 6:2225-2242(1992).
CC -1- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -1- FUNCTION: PRSH SEEMS TO ANCHOR THE PILUS TO THE BACTERIAL CELL.
CC IN ADDITION THE STOICHIOMETRIC RELATIONSHIP BETWEEN PRSH AND
CC PRSA DETERMINES THE PILUS LENGTH.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X62157; CAA44082.1; -
DR InterPro: IPR000259; Fimbrial.
DR Pfam; PF00419; Fimbrial; 1.
KW Fimbrin; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 195 PRS FIMBRIAL MINOR PILIN PROTEIN.
FT DISULFID 58 97 PROBABLE.
SQ SEQUENCE 195 AA; 21837 MW; A5065BEF93D5861B CRC64;

Query Match 10.2%; Score 6; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ARAGV 12
DB 148 ARAGV 153

RESULT 33
RMRP_YEAST STANDARD; PRT; 198 AA.
AC P40993;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RNase MRP protein component SNM1.
DE SNM1 OR YDR478W OR D8035.21.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95047399; PubMed=7958920;
RA Schmitt M.E., Clayton D.A.;
RA "Characterization of a unique protein component of yeast RNase MRP:
RA an RNA-binding protein with a zinc-cluster domain."
RL Genes Dev. 8:2617-2628(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
RA Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yelton M., Botstein D., Davis R.W.;
RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: ESSENTIAL COMPONENT OF THE MRP RIBONUCLEOPROTEIN
CC ENDORIBONUCLEASE THAT CLEAVES MITOCHONDRIAL PRIMER RNA SEQUENCES.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -----
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CC -----
DR EMBL; Z37982; CAAB6054.1; -
DR EMBL; U33050; AAB64905.1; -
DR PIR; S48236; S48236.
DR SGD: S0002866; SNM1.
KW Hydroxylase; Nuclease; RNA-binding.
FT DOMAIN 136 198 LYS/SER-RICH.
SQ SEQUENCE 198 AA; 22541 MW; 67C26258D3BEA3A CRC64;

Query Match 10.2%; Score 6; DB 1; Length 198;
```

Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 45 VVPTFG 50
122 VVPTFG 127

RESULT 34

RASM_HUMAN STANDARD; PRT; 208 AA.
ID RASM_HUMAN
AC 014807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ras-related protein M-Ras (Ras-related protein R-Ras3).
GN MRAS OR RRAS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=98062166; PubMed=9400994;
RA Kimmelman A., Tolacheva T., Lorenzi M.V., Osada M., Chan A.M.-L.,
RT Identification and characterization of R-ras3: a novel member of the
RT Ras gene family with a non-ubiquitous pattern of tissue
RT distribution.
RL Oncogene 15:2675-2686(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=99409042; PubMed=10477695;
RA Louhed J., Grasso L., de Smet C., van Roost E., Wildmann C.,
RT Interleukin-9-induced expression of M-Ras/R-Ras3 oncogene in T-helper
RT clones.
RL Blood 94:1701-1710(1999).
CC -1- FUNCTION: MAY SERVE AS AN IMPORTANT SIGNAL TRANSDUCER FOR A NOVEL
CC UPSTREAM STIMULI IN CONTROLLING CELL PROLIFERATION. WEAKLY
CC ACTIVATES THE MAP KINASE PATHWAY.
CC -1- TISSUE SPECIFICITY: EXPRESSION HIGHLY RESTRICTED TO THE BRAIN AND
CC HEART.
CC -1- INDUCTION: BY INTERLEUKIN-9, BUT NOT BY IL-2 OR IL-4.
CC -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
CC -----
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CC -----
CC EMBL: AF022080; AAC52085.1; -;
CC EMBL: AF043938; AAD02287.1; -;
CC HSSP: P01112; 1PLK.
CC InterPro: IPR003577; MRAS.
CC InterPro: IPR001230; Prenyl_site.
CC InterPro: IPR001806; Ras_trnstimng.
CC InterPro: IPR005225; Small_GTP.
CC Pfam: PF00071; ras; 1.
CC PRINTS: PR00449; RASTRNSFRMNG.
CC SMART: SM00173; RAS; 1.
CC TIGRFS: TIGR00231; small_GTP; 1.
CC GTP-binding; Prenylation; Lipoprotein.
KW NP_BIND 20 27
FT NP_BIND 67 71 GTP (BY SIMILARITY).
FT NP_BIND 126 129 GTP (BY SIMILARITY).
FT DOMAIN 42 50 EFFECTOR REGION (BY SIMILARITY).
FT DOMAIN 185 191 POLY-LYS.

FT LIPID 205 205 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 208 AA; 23846 MW; 0B2B55AFA96B3EC4 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 KKKKKT 29
185 KKKKKT 190

RESULT 35

RASM_MOUSE STANDARD; PRT; 208 AA.
ID RASM_MOUSE
AC 008989;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ras-related protein M-Ras (Ras-related protein R-Ras3) (Muscle and
DE microspikes Ras) (X-Ras).
GN MRAS OR XRAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98055615; PubMed=9395237;
RA Matsumoto K., Asano T., Endo T.,
RT Novel small GTPase M-Ras participates in reorganization of actin
RT cytoskeleton.
RL Oncogene 15:2409-2417(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=99409042; PubMed=10477695;
RA Louhed J., Grasso L., de Smet C., van Roost E., Wildmann C.,
RT Nicolaides N.C., Levitt R.C., Renaud J.-C.,
RT Interleukin-9-induced expression of M-Ras/R-Ras3 oncogene in T-helper
RT clones.
RL Blood 94:1701-1710(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Leslie K.B., Schrader J.W.,
RT Characterization of a transforming, novel ras-related molecule.
RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MAY SERVE AS AN IMPORTANT SIGNAL TRANSDUCER FOR A NOVEL
CC UPSTREAM STIMULI IN CONTROLLING CELL PROLIFERATION. WEAKLY
CC ACTIVATES THE MAP KINASE PATHWAY (BY SIMILARITY).
CC -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
CC -----
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CC -----
CC EMBL: AB004879; BAA20538.1; -;
CC EMBL: AF043581; AAD02277.1; -;
CC EMBL: AF031159; AAD01926.1; -;
CC HSSP: P01112; 1PLK.
CC MGD: MGI:1100856; Mras.
CC InterPro: IPR003577; GTPase_Ras.
CC InterPro: IPR001230; Prenyl_site.
CC InterPro: IPR001806; Ras_trnstimng.
CC InterPro: IPR005225; Small_GTP.
CC Pfam: PF00071; ras; 1.
CC PRINTS: PR00449; RASTRNSFRMNG.
CC SMART: SM00173; RAS; 1.
CC TIGRFS: TIGR00231; small_GTP; 1.

KM GTP-binding; Prenylation; Lipoprotein.
 FT NE_BIND 20 27 GTP (BY SIMILARITY).
 FT NE_BIND 67 71 GTP (BY SIMILARITY).
 FT NE_BIND 126 129 GTP (BY SIMILARITY).
 FT DOMAIN 42 50 EFFECTOR REGION (BY SIMILARITY).
 FT DOMAIN 185 191 POLY-LYS.
 FT LIPID 205 205 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 208 AA; 23901 MW; 975CFDD1FDF37FCF CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKK 29
 185 KKKKK 190

Db 185 KKKKK 190

RESULT 36
 RASM RAT
 ID RASM RAT STANDARD; PRT; 208 AA.
 AC P97538; 009021; (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ras-related protein M-Ras (Ras-related protein R-Ras3).
 GN M-RAS OR R-RAS3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98055615; PubMed=9395237;
 RA Matsuno K., Asano T., Endo T.;
 RT "Novel small GTPase M-Ras participates in reorganization of actin
 cytoskeleton.";
 RL Oncogene 15:2409-2417(1997).
 RN [2]
 RP REVISION TO 136.
 RA Endo T.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY SERVE AS AN IMPORTANT SIGNAL TRANSDUCER FOR A NOVEL
 UPSTREAM STIMULI IN CONTROLLING CELL PROLIFERATION. WEAKLY
 ACTIVATES THE MAP KINASE PATHWAY (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE CELLS.
 CC -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
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 or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; D89863; BAA20531.1; -
 DR HSSP; P01112; IPLK.
 DR InterPro: IPR003577; GTPase_Ras.
 DR InterPro: IPR001230; Prenyl_site.
 DR InterPro: IPR001806; Ras_tnsfrmg.
 DR InterPro: IPR005225; Small_GTP.
 DR Pfam; PF00071; Ras; 1.
 DR PRINTS; PR00449; RASTRNSFRMG.
 DR SMART; SM00173; Ras; 1.
 DR TIGRFAMs; TIGR00231; small_gtp; 1.
 KM GTP-binding; Prenylation; Lipoprotein.
 FT NE_BIND 20 27 GTP (BY SIMILARITY).
 FT NE_BIND 67 71 GTP (BY SIMILARITY).
 FT NE_BIND 126 129 GTP (BY SIMILARITY).
 FT DOMAIN 42 50 EFFECTOR REGION (BY SIMILARITY).
 FT DOMAIN 185 191 POLY-LYS.

FT LIPID 205 205 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 208 AA; 23887 MW; 0869627A12C67E8A CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKK 29
 185 KKKKK 190

Db 185 KKKKK 190

RESULT 37
 RISA BUCAI
 ID RISA BUCAI STANDARD; PRT; 208 AA.
 AC P57212;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Riboflavin synthase alpha chain (EC 2.5.1.9).
 GN RIBE OR BU112
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Matsumoto H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. APS.";
 RL Nature 407:81-86(2000).
 CC -1- FUNCTION: RIBOFLAVIN SYNTHASE IS A BIFUNCTIONAL ENZYME COMPLEX
 CATALYZING THE FORMATION OF RIBOFLAVIN FROM 5-AMINO-6-(1'-D)-
 RIBITYL-AMINO-2,4(1H,3H)-PYRIMIDINEDIONE AND L-3,4-DIHYDROXY-2-
 BUTANONE-4-PHOSPHATE VIA 6,7-DIMETHYL-8-LUMAZINE. THE ALPHA
 SUBUNIT CATALYZES THE DISMUTATION OF 6,7-DIMETHYL-8-LUMAZINE TO
 RIBOFLAVIN AND 5-AMINO-6-(1'-D)-RIBITYL-AMINO-2,4(1H,3H)-
 PYRIMIDINEDIONE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2,6,7-dimethyl-8-(1'-D-ribityl)lumazine -
 riboflavin + 4-(1'-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
 CC -1- PATHWAY: FINAL STEPS OF RIBOFLAVIN SYNTHESIS.
 CC -1- SUBUNIT: OLIGOMER THAT CONSIST OF 3 ALPHA SUBUNITS AND 60 BETA
 SUBUNITS (BY SIMILARITY).
 CC -1- SIMILARITY: TO BIOLUMINESCENCE ANTENNA PROTEINS LUXY (YFP) AND
 LUXL (LUMP).
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 CC -----
 CC EMBL; AP001118; BAB12830.1; -
 DR InterPro: IPR001783; Lum_binding.
 DR Pfam; PF00677; Lum_binding; 2.
 DR ProDom; PD004110; Lum_binding; 2.
 DR TIGRFAMs; TIGR00187; ribe; 1.
 DR PROSITE; PS00693; LUM_BINDING; FALSE_NEG.
 KM Riboflavin biosynthesis; Transference; Repeat; Complete proteome.
 FT REPEAT 1 97
 FT REPEAT 98 201
 FT SITE 81 85 BINDS TO LUMAZINE (PROBABLE).
 FT SITE 179 183 BINDS TO LUMAZINE (PROBABLE).
 SQ SEQUENCE 208 AA; 23505 MW; 7CCE3272CF54BA5B CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKK 28
Db 16 EKKKKK 21

RESULT 38
RHO1_YEAST STANDARD: PRT; 209 AA.
AC P06780;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RHO1 protein.
GN RHO1 OR YPR165W OR P9325.3.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetiales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxId=4932;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-87118248; PubMed-3543936;
RA Madale P., Axel R., Myers A.M.;
RT "Characterization of two members of the rho gene family from the
RT yeast Saccharomyces cerevisiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:779-783(1987).
RL [2]
RN SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RX MEDLINE-97313271; PubMed-9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoorge W.,
RA Ardujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA Borteln D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Dillus H., DiPaolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Fleetham M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
RA Hunnicke-Smith S., Hyman R., Johnston M., Kaiman S., Kleene K.,
RA Komp C., Kirdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Martche R., Messenguy F., Mewes H.-W., Miliptat S., Moestl D.,
RA Mueller-Auer S., Namath A., Neutwich U., Oefner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharte M.,
RA Scherens B., Schramm S., Schroeder M., Sidic A.M., Tettelin H.,
RA Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
RA Walsh S.V., Wambolt R., Wang Y., Wedler E., Wedler H., Winnelt E.,
RA Zhong W.W., Zollner A., Vo D.H., Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL Nature 387:103-105(1997).
RN [3]
RN SEQUENCE OF 201-209 FROM N.A.
RX MEDLINE-87137621; PubMed-3029111;
RA Myers A.M., Crivellone M.D., Tzagoloff A.;
RT "Assembly of the mitochondrial membrane system. MRP1 and MRP2, two
RT yeast nuclear genes coding for mitochondrial ribosomal proteins.";
RL J. Biol. Chem. 262:3388-3397(1987).
CC -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
CC
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CC
CC EMBL: M15189; AAA34977.1; -;
DR EMBL: U25840; AAB68152.1; -;
DR EMBL: M15161; AAA4729.1; -;
DR PIR: A26587; TVBYH1.
DR HSSP: P06749; 1FTN.
DR SGD: S0006369; RHO1.
DR InterPro: IPR003578; GTPase_Rho.
DR InterPro: IPR001230; Prenyl_site.
DR InterPro: IPR001806; Ras_transfiring.

DR InterPro: IPR005225; Small_GTP.
DR Pfam: PF00071; ras.1.
DR PRINTS: PR00449; RASTRNSFRMNG.
DR SMART: SM00174; RHO.1.
DR TIGRfams: TIGR00231; small_GTP.1.
KW GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 17 24 GTP (BY SIMILARITY).
FT NP_BIND 64 68 GTP (BY SIMILARITY).
FT NP_BIND 122 125 GTP (BY SIMILARITY).
FT DOMAIN 39 47 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 206 206 GERANYL-GERANYL.
SQ SEQUENCE 209 AA; 23152 MW; 630B17E9E34CE75 CRC64;
Query Match 10.2%; Score 6; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 23 EKKKKK 28
Db 200 EKKKKK 205

RESULT 39
T402_BURCE STANDARD: PRT; 211 AA.
ID T402_BURCE
AC P24536;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative transposase for insertion sequence element IS402.
OS Burkholderia cepacia (Pseudomonas cepacia).
OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC Burkholderia.
OX NCBI_TaxId=292;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-91323723; PubMed-1650732;
RA Ferrante A.A., Lessie T.G.;
RT "Nucleotide sequence of IS402 from Pseudomonas cepacia.";
RL Gene 102:143-144(1991).
CC -!- FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION
CC SEQUENCE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 13.
CC
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CC
CC EMBL: M64065; -; NOT_ANNOTATED_CDS.
DR PIR: J01133; J01133.
DR InterPro: IPR002559; Transposase_11.
DR Pfam: PF01609; Transposase_11.1.
KW Hypothetical protein; Transposase element; Transposition;
KW DNA-binding; DNA recombination.
SQ SEQUENCE 211 AA; 23968 MW; A5DC9696A1EA820B CRC64;
Query Match 10.2%; Score 6; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 GSLARA 9
Db 21 GSLARA 26

RESULT 40
KSL_HYDAT
ID KSL_HYDAT STANDARD: PRT; 217 AA.
AC P38978;

```

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE KSI protein precursor (Head-specific protein 1) (Kopf-spezifisches
DE protein 1).
GN KSI.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95044930; PubMed=7956827;
RA Weinberger R., Salgado L.M., David C.N., Bosch T.C.G.;
RT "Ksl, an epithelial cell-specific gene, responds to early signals of
RT head formation in Hydra."
RL Development 120:2511-2517(1994).
CC -1- FUNCTION: RESPONDS TO EARLY SIGNALS OF HEAD FORMATION IN HYDRA.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN TENTACLE-SPECIFIC EPITHELIAL
CC CELLS (BATTERY CELLS) AS WELL AS IN A SMALL FRACTION OF ECTODERMAL
CC EPITHELIAL CELLS IN THE GASTRIC REGION SUBJACENT TO THE TENTACLES
CC (THE TENTACLE FORMATION REGION). THE LATER CELLS ARE COMMITTED TO
CC BECOME BATTERY CELLS.
CC -1- INDUCTION: BY PKC.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X78596; CA55331.1; -
DR PIR: S43193; S43193.
KW Developmental protein; Signal; Repeat.
FT SIGNAL 1 16
FT CHAIN 17 217
FT DOMAIN 32 147
FT REPEAT 32 81
FT REPEAT 98 147
FT DOMAIN 32 45
FT DOMAIN 47 96
FT DOMAIN 97 111
FT DOMAIN 113 147
FT DOMAIN 148 217
SQ SEQUENCE 217 AA; 25427 MW; 0010423D1364B48 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
DB 96 EKKKKK 101

RESULT 41
FLIZ_BACSU
AC P35336; STANDARD; PRT; 219 AA.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Flagellar biosynthetic protein fliz precursor.
GN FLIZ OR CHEA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=168 / OT1085;
RX MEDLINE=92283757; PubMed=1597417;

```

```

RA Bischoff D.S., Weinreich M.D., Ordal G.W.;
RT "Nucleotide sequences of Bacillus subtilis flagellar biosynthetic
RT genes fliz and fliz0 and identification of a novel flagellar gene,
RT fliz."
RL J. Bacteriol. 174:4017-4025(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertorello M.G., Bessières P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Bridnell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devylen K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Enlian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallazzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollubly E.J., Grand G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaert-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Médigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Portetelle S., Prescott A.M.,
RA Prescan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Takashashi A., Tanaka T., Terstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vamler F., Vassarotti A.,
RA Viari A., Wamboldt R., Wedler E., Wedler H., Weitzenger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -1- FUNCTION: MAY BE A STRUCTURAL COMPONENT OF THE FLAGELLUM THAT
CC ANCHORS THE ROD TO THE MEMBRANE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M87005; AAA22452.1; -
DR EMBL: Z99112; CAB13507.1; -
DR PIR: B41886; B41886.
DR Subtilist; BG10259; fliz.
KW Flagella; Signal; Transmembrane; Complete proteome.
FT SIGNAL 1 26
FT CHAIN 27 219
FT TRANSMEM 71 96
SQ SEQUENCE 219 AA; 24871 MW; 6FE82AF8E1DAEE8 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 219;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GKRRKP 55
DB 210 GKRRKP 215

RESULT 42
UNG_BUCAI

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ID  UNG_BUCAL          STANDARD:          PRT:          220 AA.
AC  P57280;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DE  16-OCT-2001 (Rel. 40, Last annotation update)
DE  uracil-DNA glycosylase (EC 3.2.2.-) (UDG).
GN  UNG OR BU183.
OS  Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS  symbiotic bacterium).
OC  Bacteria: Proteobacteria: gamma subdivision: Buchnera.
OX  NCBI_TaxID=118099;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Tokyo 1998;
RC  MEDLINE=20445173; PubMed=10993077;
RT  Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT  "Genome sequence of the endocellular bacterial symbiont of aphids
RT  Buchnera sp. APS."
RL  Nature 407:81-86(2000).
CC  -1- FUNCTION: EXCISES URACIL RESIDUES FROM THE DNA WHICH CAN ARISE
CC  AS A RESULT OF MISINCORPORATION OF DUMP RESIDUES BY DNA
CC  POLYMERASE OR DUE TO DEAMINATION OF CYTOSINE (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -1- SIMILARITY: BELONGS TO THE URACIL-DNA GLYCOSYLASE FAMILY.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: AF001118; BAB12900.1; -
DR  HSSP: P12295; 1EUG.
DR  InterPro: IPR005122; UDNA_glycos.
DR  InterPro: IPR002043; U_DNA_glycosylase.
DR  InterPro: IPR003249; U_glycosyl.
DR  Pfam: PF03167; UDG; 1.
DR  ProDom: PD001589; U_glycosyl; 1.
DR  TIGRfam: TIGR00628; ung; 1.
DR  PROSITE: PS00130; U_DNA_GLYCOSYLASE; 1.
KW  DNA repair; Hydrolase; Glycosidase; Complete proteome.
FT  ACT_SITE 61 61  GENERAL BASE (BY SIMILARITY).
SQ  SEQUENCE 220 AA; 25653 MW; AEAFL9BEE0A2942C CRC64;

Query Match          10.2%; Score 6; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  22 QEKKK 27
    |||||
DB  11 QEKKK 16

RESULT 43
RS3A_PYRAE          STANDARD:          PRT:          221 AA.
ID  RS3A_PYRAE
AC  O82721;
DT  15-JUN-2002 (Rel. 41, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  30S ribosomal protein S3ae.
GN  RPS3AE OR PAE3472.
OS  Pyrobaculum aerophilum.
OC  Archaea: Crenarchaeota: Thermoprotei; Thermoproteales;
OC  Thermoproteaceae; Pyrobaculum.
OX  NCBI_TaxID=13773;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=IM2 / ATCC 51768 / DSM 7523;
RC  PubMed=11792869;
RA  Fitz-Gibbon S.T., Ladner H., Kim D.-J., Stetter K.O., Simon M.I.,

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RA  Miller J.H.;
RT  "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT  aerophilum.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
CC  -1- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RIBOSOMAL PROTEINS.
CC  -----
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CC  -----
DR  EMBL: AE009933; AAL64942.1; -
DR  InterPro: IPR001593; Ribosomal_S3AE.
DR  Pfam: PF01015; Ribosomal_S3AE; 1.
DR  ProDom: PD003035; Ribosomal_S3AE; 1.
DR  PROSITE: PS01191; RIBOSOMAL_S3AE; FALSE_NEG.
KW  Ribosomal protein; Complete proteome.
SQ  SEQUENCE 221 AA; 24761 MW; 19F91730136136AA CRC64;

Query Match          10.2%; Score 6; DB 1; Length 221;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  19 VAKQK 24
    |||||
DB  8 VAKQK 13

RESULT 44
YJ08_YEAST
ID  YJ08_YEAST          STANDARD:          PRT:          233 AA.
AC  P47006;
DT  01-FEB-1996 (Rel. 33, Created)
DT  01-FEB-1996 (Rel. 33, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last annotation update)
DE  Hypothetical 26.9 kDa protein in INO1-ID52 intergenic region.
GN  YJ148W OR J0637.
OS  Saccharomyces cerevisiae (Baker's yeast).
OC  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC  Saccharomycetales; Saccharomycetaceae; Saccharomycas.
OX  NCBI_TaxID=4932;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=S288c / FY1679;
RC  MEDLINE=96408771; PubMed=8913765;
RA  Katsoulou C., Tzeremia M., Tavernarakis N., Alexandraki D.;
RT  "Sequence analysis of a 40.7 kb segment from the left arm of yeast
RT  chromosome X reveals 14 known genes and 13 new open reading frames
RT  including homologues of genes clustered on the right arm of
RT  chromosome XI."
RL  Yeast 12:787-797(1996).
CC  -----
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CC  -----
DR  EMBL: Z49423; CAA89443.1; -
DR  EMBL: X87371; CAA50807.1; -
DR  SGD: S0003684; YJ148W.
KW  Hypothetical protein.
FT  DOMAIN 184 233  GLU/LYS-RICH.
FT  DOMAIN 208 215  POLY-LYS.
FT  DOMAIN 221 230
SQ  SEQUENCE 233 AA; 26875 MW; DCD42DEEC574EDB6 CRC64;

Query Match          10.2%; Score 6; DB 1; Length 233;

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Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 6, 2003, 21:31:12
Job time : 14 secs

OY 23 EKKKKR 28
|||||
DB 207 EKKKKR 212

RESULT 45

CAVL_CAEEL STANDARD; PRT; 235 AA.
ID CAVL_CAEEL
AC Q94051;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Caveolin-1.
OS CAV-1 OR T13F2.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RX MEDLINE=97153022; PubMed=8999956;
RA Tang Z., Okamoto T., Boontrakulpoontawe P., Katada T., Otsuka A.J.,
RA Lisanti M.P.,
RT "Identification, sequence, and expression of an invertebrate caveolin
RT gene family from the nematode Caenorhabditis elegans. Implications
RT for the molecular evolution of mammalian caveolin genes.";
RL J. Biol. Chem. 272:2437-2445(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Swindburne J.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MAY ACT AS A SCAFFOLDING PROTEIN WITHIN CAVEOLAR
CC MEMBRANES. INTERACTS DIRECTLY WITH G-PROTEIN ALPHA SUBUNITS AND
CC CAN FUNCTIONALLY REGULATE THEIR ACTIVITY.
CC -1- SUBUNIT: HOMOLIGOMER CONTAINING 14-16 MONOMERS PER OLIGOMER.
CC -1- SUBCELLULAR LOCATION: MEMBRANE PROTEIN OF CAVEOLAE. POTENTIAL
CC HAIRPIN-LIKE STRUCTURE IN THE MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CAVEOLIN FAMILY.
CC
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CC
CC
CC EMBL: U66405; AAB48388.1; -
CC EMBL: Z81122; CAB03359.1; -
CC WormPep: T13F2.8; CEL3633.
CC InterPro: IPR001612; Caveolin.
CC Pfam: PF01146; Caveolin.1.
CC PROSITE: PS01210; CAVEOLIN; FALSE-NEG.
KW Transmembrane; Lipoprotein; Palmitate.
FT DOMAIN 1 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 182 POTENTIAL.
FT DOMAIN 183 235 CYTOPLASMIC (POTENTIAL).
FT LIPID 234 234 PALMITATE (POTENTIAL).
SQ SEQUENCE 235 AA: 26291 MW; F07B12DEB4D6F13A CRC64;

Query Match 10.2%; Score 6; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 TFGKKK 53
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DB 46 TFGKKK 51


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; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 479
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-479

Query Match          10.2%; Score 6; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
    |||||
Db 35 EKKKKK 40

RESULT 24
US-09-764-869-1228
; Sequence 1228, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1228
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-869-1228

Query Match          10.2%; Score 6; DB 10; Length 52;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKK 29
    |||||
Db 9 KKKKKK 14

RESULT 25
US-09-764-855-113
; Sequence 113, Application US/09764855
; Patent No. US20020119919A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA110
; CURRENT APPLICATION NUMBER: US/09/764,855
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 113
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
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; LOCATION: (19)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-764-855-113

Query Match          10.2%; Score 6; DB 10; Length 55;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
    |||||
Db 48 EKKKKK 53

RESULT 26
US-09-764-847-601
; Sequence 601, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 601
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-847-601

Query Match          10.2%; Score 6; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
    |||||
Db 45 EKKKKK 50

RESULT 27
US-09-864-761-47593
; Sequence 47593, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
; FILE REFERENCE: Acomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47593
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALO49694.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN HB100, SIGNAL = 0.88
; OTHER INFORMATION: SWISSPROT HIT: P13866, EVALU8 5.00e-14
; OTHER INFORMATION: EST_HUMAN HIT: BE344101.1, EVALU8 8.00e-18
; US-09-864-761-47593
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Query Match 10.2%; Score 6; DB 10; Length 57;
Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 RCGTPK 18
Db 6 RCGTPK 11

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RESULT 28
; US-09-864-761-47812
; Sequence 47812, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47812
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010290.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.51
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
; OTHER INFORMATION: EST_HUMAN HIT: BE244981.1, EVALU8 1.00e-12
; US-09-864-761-47812
```

Query Match 10.2%; Score 6; DB 10; Length 59;
Best Local Similarity 100.0%; Pred. No. 32;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
Db 16 EKKKK 21

```
RESULT 29
; US-09-989-919-118
; Sequence 118, Application US/09989919
; Patent No. US20020164344A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Heve
; APPLICANT: Pluta, Jason
; APPLICANT: Ghosh, Malavika
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and
; FILE REFERENCE: DEX-0289
; CURRENT APPLICATION NUMBER: US/09/989,919
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,505
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-989-919-118
```

Query Match 10.2% Score 6; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||

Db 54 EKKKK 59

RESULT 30
US-09-925-300-1198
; Sequence 1198, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1198
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1198

Query Match 10.2% Score 6; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||

Db 53 EKKKK 58

RESULT 31
US-09-925-301-1475
; Sequence 1475, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1475
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (9)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (48)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1475

Query Match 10.2% Score 6; DB 10; Length 62;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||

Db 36 EKKKK 41

RESULT 32
US-10-117-604-2
; Sequence 2, Application US/10117604
; Patent No. US20020168672A1
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING
; SCHWANNOMIN-BINDING-PROTEINS AND PRODUCTS RELATED THEREBY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/117,604
; FILING DATE: 04-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,089
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/030,987
; FILING DATE: 15-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramos, Robert T.
; REGISTRATION NUMBER: 37,915
; REFERENCE/DOCKET NUMBER: P-CE 2862
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-117-604-2

Query Match 10.2% Score 6; DB 9; Length 63;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28

Db 15 EKKKKK 20

RESULT 33

US-09-764-846-260
; Sequence 260, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 260
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-846-260

Query Match 10.2%; Score 6; DB 10; Length 63;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 EKKKKK 28
Db 25 EKKKKK 30

RESULT 34

US-09-864-761-45501
; Sequence 45501, Application US/09864761
; Patent No. US2002048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45501
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008739.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.56
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
US-09-864-761-45501

Query Match 10.2%; Score 6; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 EKKKKK 28
Db 51 EKKKKK 56

RESULT 35

US-09-764-846-224
; Sequence 224, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-846-224

Query Match 10.2%; Score 6; DB 10; Length 66;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 EKKKKK 28
Db 39 EKKKKK 44

RESULT 36

US-09-764-877-1089
; Sequence 1089, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1089
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-877-1089

Query Match 10.2%; Score 6; DB 10; Length 66;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKT 29
|||||
DB 56: KKKKKT 61

RESULT 37
US-09-867-550-284
Sequence 284, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:

APPLICANT: Leach, Martin D.
APPLICANT: Mehrabad, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 284
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-867-550-284

Query Match 10.2%; Score 6; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TFGKKK 53
|||||
DB 28 TFGKKK 33

RESULT 38
US-09-201-936-18
Sequence 18, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-18

Query Match 10.2%; Score 6; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 10
|||||
DB 21 SLARAG 26

RESULT 39
US-09-201-936-19
Sequence 19, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-19

Query Match 10.2%; Score 6; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 10
|||||
DB 21 SLARAG 26

RESULT 40
US-09-764-846-191
Sequence 191, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT212
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 191
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

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; NAME/KEY: SITE
; LOCATION: (66)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-846-191
```

```
Query Match          10.2%; Score 6; DB 10; Length 68;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 23 EKKKKK 28
    |||||
Db 37 EKKKKK 42
```

RESULT 41

```
US-09-925-299-1340
; Sequence 1340, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1340
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (65)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (69)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1340
```

```
Query Match          10.2%; Score 6; DB 10; Length 69;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 23 EKKKKK 28
    |||||
Db 19 EKKKKK 24
```

RESULT 42

```
US-09-764-846-179
; Sequence 179, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
```

```
; CURRENT FILING DATE: 2001-01-17
; APPLICATION DATA removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-846-179
```

```
Query Match          10.2%; Score 6; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 23 EKKKKK 28
    |||||
Db 53 EKKKKK 58
```

RESULT 43

```
US-09-925-300-1105
; Sequence 1105, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1880
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1105
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (65)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (69)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1105
```

```
Query Match          10.2%; Score 6; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 23 EKKKKK 28
    |||||
Db 55 EKKKKK 60
```

RESULT 44

```
US-09-764-846-242
; Sequence 242, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 242
; LENGTH: 73
```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-846-242

Query Match 10.2%; Score 6; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
|||||
DB 40 EKKKKK 45

RESULT 45
US-09-833-067-9
; Sequence 9, Application US/09833067
; Patent No. US2002005488A1
; GENERAL INFORMATION:
; APPLICANT: O'HANLEY, PETER
; APPLICANT: DENICH, KENNETH
; TITLE OF INVENTION: DISSOCIATED PILL, THEIR PRODUCTION AND USE
; FILE REFERENCE: 050939/0102
; CURRENT APPLICATION NUMBER: US/09/833,067
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/196,493
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentl Ver. 2.1
; SEQ ID NO 9
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of papH gene deletion mutant
US-09-833-067-9

Query Match 10.2%; Score 6; DB 10; Length 75;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ARAGKV 12
|||||
DB 26 ARAGKV 31

Search completed: February 6, 2003, 21:32:50
Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 21:30:34 ; Search time 18 Seconds
(without alignments)
315.107 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59
Sequence: 1 KVGSLARAGKVRGQTPKVA.....RRFVNVVPTFGKKKGPNNNS 59

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	133	1 A47416	ubiquitin-like pro
2	59	100.0	133	2 JC1278	ubiquitin-like pro
3	59	100.0	133	2 I48346	ribosomal protein
4	22	37.3	62	2 H85342	RIBOSOMAL PROTEIN
5	22	37.3	68	2 F84580	40S ribosomal prot
6	20	33.9	229	2 S38383	SEB4B protein - hu
7	13	22.0	130	2 T15642	hypothetical prote
8	12	20.3	58	2 A71604	ribosomal protein
9	12	20.3	61	2 T39834	ribosomal protein
10	12	20.3	63	1 S67074	ribosomal protein
11	8	13.6	135	2 A97094	uncharacterized pr
12	7	11.9	134	2 S02776	DNA-binding protei
13	7	11.9	154	2 B75305	hypothetical prote
14	7	11.9	199	2 E84782	probable homeodoma
15	7	11.9	215	2 T52523	nucleoporin p52 ho
16	7	11.9	233	2 H86318	protein 60S riboso
17	7	11.9	233	2 D96768	protein 60S riboso
18	7	11.9	233	2 E96768	protein 60S riboso
19	7	11.9	283	2 T47174	hypothetical prote
20	7	11.9	314	2 D70313	riboflavin kinase
21	7	11.9	346	2 T19629	hypothetical prote
22	7	11.9	424	2 T36154	probable ABC-type
23	7	11.9	454	2 E84153	replicative DNA he
24	7	11.9	710	2 T49516	Altu related prote
25	7	11.9	863	2 F85343	hypothetical prote
26	7	11.9	1254	1 J031979	structural polypor
27	7	11.9	2539	2 B71619	hypothetical prote
28	6	10.2	46	2 T28799	hypothetical prote
29	6	10.2	67	2 B69830	hypothetical prote

30	6	10.2	70	2 H97135	uncharacterized ph
31	6	10.2	74	2 T47434	hypothetical prote
32	6	10.2	80	2 B82267	exodeoxyribonuclea
33	6	10.2	81	2 S66013	ribosomal protein
34	6	10.2	92	2 T36134	hypothetical prote
35	6	10.2	92	2 H82867	transcription regu
36	6	10.2	98	2 H96585	hypothetical prote
37	6	10.2	102	2 T07078	cold stress protei
38	6	10.2	104	2 C87604	virulence-associat
39	6	10.2	105	2 PM0017	hypothetical prote
40	6	10.2	105	2 PM0018	hypothetical prote
41	6	10.2	106	2 S59536	cold stress protei
42	6	10.2	115	2 S69849	hypothetical prote
43	6	10.2	117	2 H84651	hypothetical prote
44	6	10.2	123	2 B71268	probable ribosomal
45	6	10.2	125	1 R3RT25	ribosomal protein

ALIGNMENTS

```
RESULT 1
A47416
N:Contains: ribosomal protein / ribosomal protein S30, cytosolic [validated] - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: A47416; B47416; S18101
R:Olvera, J.; Wool, I.G.
J. Biol. Chem. 268, 17967-17974, 1993
A>Title: The carboxyl extension of a ubiquitin-like protein is rat ribosomal protein
A:Reference number: A47416; MUID:93352612; PMID:8394356
A:Accession: A47416
A:Molecule type: mRNA
A:Residues: 1-133 <OLV>
A:Cross-references: EMBL:X62671; NID:g407165; PIDN:CAA44545.1; PID:g57566
A:Accession: B47416
A:Molecule type: protein
A:Residues: 75-92 <OL2>
A>Note: the proteins are designated as ubiquitin-like protein and ribosomal protein &
C:Keywords: protein biosynthesis; ribosome
F:1-74/Product: ubiquitin-like protein #status predicted <UBI>
F:75-133/Product: ribosomal protein S30 #status experimental <RIB>

Query Match          100.0%; Score 59; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 5, 2e-52;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVRGQTPKVAQKKKKTKGRARRRQYNNRFVNVVPTFGKKKGPNNNS 59
DB 75 KVGSLARAGKVRGQTPKVAQKKKKTKGRARRRQYNNRFVNVVPTFGKKKGPNNNS 133

RESULT 2
JC1278
N:Alternate names: fau protein
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Sep-1999
C:Accession: JC1278; I37387; S68911; S21449; S21450
R:Kas, K.; Michiels, L.; Merregaert, J.
Biochem. Biophys. Res. Commun. 187, 927-933, 1992
A>Title: Genomic structure and expression of the human fau gene: Encoding the ribosomal
A:Reference number: JC1278; MUID:92412144; PMID:1326960
A:Accession: JC1278
A:Molecule type: DNA
A:Residues: 1-133 <KAS>
A:Cross-references: EMBL:X65921; NID:g31304; PIDN:CAA46714.1; PID:g31305
R:Michiels, L.; Van der Raaij-Waelt, E.; Van Hasselt, F.; Kas, K.; Merregaert, J.
Oncogene 8, 2537-2546, 1993
A>Title: fau cDNA encodes a ubiquitin-like-S30 fusion protein and is expressed as an
```

A:Reference number: I37387; MUID:93368957; PMID:8395683
A:Accession: I37387
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133 <RES>
A:Cross-references: EMBL:X65923; NID:g31302; PIDN:CAA46716.1; PID:g31303
R.Vladimirov, S.N.; Ivanov, A.V.; Karpova, G.G.; Musolyamov, A.K.; Egorov, T.A.; Thiede, Eur. J. Biochem. 239, 144-149, 1996
A:Title: Characterization of the human small-ribosomal-subunit proteins by N-terminal ar
A:Reference number: S68911; MUID:96305378; PMID:8706699
A:Accession: S68911
A:Molecule type: protein
A:Residues: 75-99 <VLA>
C:Genetics:
A:Gene: fau
A:Introns: 25/3; 74/1; 92/3
C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
C:Keywords: protein biosynthesis; ribosome
F:1-74/Domain: ubiquitin homology <UBH>
F:75-133/Product: ribosomal protein S30, cytosolic #status experimental <MAT>

Query Match 100.0%; Score 59; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.2e-52;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVRGOTPKYAKOEKKKKTKGRARRRQYRRFVNVPTFGKKKGPYANS 59
Db 75 KVGSLARAGKVRGOTPKYAKOEKKKKTKGRARRRQYRRFVNVPTFGKKKGPYANS 133

RESULT 3
148346
ribosomal protein fau - mouse
N:Alternate names: gene fau protein; monoclonal nonspecific suppressor factor beta
C:Species: Mus musculus (house mouse)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Sep-1999
C:Accession: I48346; A56532; I59368; S21452
R.Michiels, L.; Van der Raueelaert, E.; Van Hasselt, F.; Kas, K.; Merregaert, J.
Oncogene 8, 2537-2546, 1993
A:Title: fau cDNA encodes a ubiquitin-like-S30 fusion protein and is expressed as an an
A:Reference number: I37387; MUID:93368957; PMID:8395683
A:Accession: I48346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133 <RES>
A:Cross-references: EMBL:X65922; NID:g50949; PIDN:CAA46715.1; PID:g50950
R.Casteels, D.; Portier, C.; Guenet, J.L.; Merregaert, J.
Genomics 25, 291-294, 1995
A:Title: The mouse fau gene: genomic structure, chromosomal localization, and characteri
A:Reference number: A56532; MUID:95293388; PMID:7774934
A:Accession: A56532
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <CAS>
A:Cross-references: GB:I33715; NID:g497610; PIDN:AAA91564.1; PID:g497611
A:Note: authors translated the codon GGT for residue 119 as Atg, and GTC for residue 120
R.Nakamura, M.; Xavier, R.M.; Tsunematsu, T.; Tanigawa, Y.
Proc. Natl. Acad. Sci. U.S.A. 92, 3463-3467, 1995
A:Title: Molecular cloning and characterization of a cDNA encoding monoclonal nonspecific
A:Reference number: I59368; MUID:95241522; PMID:7724584
A:Accession: I59368
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133 <RES>
A:Cross-references: GB:D26610; NID:g1060926; PIDN:BAA05655.1; PID:g1060927
C:Genetics:
A:Gene: fau
A:Introns: 25/3; 74/1; 92/3
C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
F:1-74/Domain: ubiquitin homology <UBH>

Query Match 100.0%; Score 59; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.2e-52;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVRGOTPKYAKOEKKKKTKGRARRRQYRRFVNVPTFGKKKGPYANS 59
Db 75 KVGSLARAGKVRGOTPKYAKOEKKKKTKGRARRRQYRRFVNVPTFGKKKGPYANS 133

RESULT 4
H85342
RIBOSOMAL PROTEIN S30 homolog [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: H85342
R.anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: H85342
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <STO>
A:Cross-references: GB:NC_001268; NID:g7269837; PIDN:CAB79697.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4G29390
A:Map position: 4

Query Match 37.3%; Score 22; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.3e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVRGOTPKYAKQ 22
Db 3 KVGSLARAGKVRGOTPKYAKQ 24

RESULT 5
F84580
40S ribosomal protein S30 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C:Accession: F84580
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84580
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <STO>
A:Cross-references: GB:AE002093; NID:g3687243; PIDN:AAC62141.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g19750
A:Map position: 2
C:Superfamily: yeast ribosomal protein S30.e

Query Match 37.3%; Score 22; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 4.7e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVRGOTPKYAKQ 22
Db 9 KVGSLARAGKVRGOTPKYAKQ 30

RESULT 6
S38383
SBB4B protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 08-Sep-1997
C:Accession: S38383
R.Ruehlmann, A.; Gupta, A.; Terworst, C.

submitted to the EMBL Data Library, September 1993
A:Description: A novel murine RRM-type protein and its human homolog.

A:Reference number: S38382

A:Accession: S38383

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-229 <RUE>

A:Cross-references: EMBL:X75315

C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein
F:25-91/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match

Best Local Similarity 33.9%; Score 20; DB 2; Length 229;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 RMQYRRRVNVVPFGKKKG 54

Db 1 RMQYRRRVNVVPFGKKKG 20

RESULT 7

T15642

hypothetical protein C26F1.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999

C:Accession: T15642

R:Geisels, C.; Stellev, L.; Bradshaw, H.

submitted to the EMBL Data Library, March 1996

A:Description: The sequence of *C. elegans* cosmid C26F1.

A:Reference number: Z18381

A:Accession: T15642

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-130 <GEI>

A:Cross-references: EMBL:U53148; NID:g1255375; PID:g1255381; PIDN:AAB37076.1; GSPDB:GN0C

A:Experimental source: strain Bristol NZ; clone C26F1

C:Genetics:

A:Gene: CESP:C26F1.4

A:Map position: 5

A:Introns: 27/3; 71/1

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match

Best Local Similarity 22.0%; Score 13; DB 2; Length 130;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSRLARAKVR 13

Db 72 KVHGSRLARAKVR 84

RESULT 8

A71604

ribosomal protein S30 PFB0885w - malaria parasite (*Plasmodium falciparum*)

C:Species: *Plasmodium falciparum*

C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 13-Aug-1999

C:Accession: A71604

R:Gardner, M.J.; Tettein, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;

; Ferreira, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.

Science 282, 1126-1132, 1998

A:Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.

A:Reference number: A71600; MUID:99021743; PMID:9804551

A:Accession: A71604

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-58 <GAR>

A:Cross-references: GB:AE001422; GB:AE001362; NID:g3845298; PIDN:AAC71966.1; PID:g384530

A:Experimental source: clone 307

C:Genetics:

A:Gene: PFB0885w

C:Superfamily: yeast ribosomal protein S30.e

Query Match

20.3%; Score 12; DB 2; Length 58;

Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSRLARAKVR 12

Db 3 KVHGSRLARAKVR 14

RESULT 9

T39834

ribosomal protein s30 - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000

C:Accession: T39834

R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.

submitted to the EMBL Data Library, February 1998

A:Accession: T39834

A:Reference number: Z21884

A:Molecule type: DNA

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-61 <LYN>

A:Cross-references: EMBL:AL021839; PIDN:CAA17057.2; GSPDB:GN00067; SPDB:SPBC1967.03c

A:Experimental source: strain 972h-; cosmid c1967

C:Genetics:

A:Gene: SPDB:SPBC1967.03c

A:Map position: 2

A:Introns: 13/3; 56/3

C:Superfamily: yeast ribosomal protein S30.e

Query Match

Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSRLARAKVR 12

Db 3 KVHGSRLARAKVR 14

RESULT 10

S67074

ribosomal protein S30.e, cytosolic - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: protein O4725; protein YLR287c-a; protein YOR182c

C:Species: *Saccharomyces cerevisiae*

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: S67074; S70775; S70776; S70774

R:Hughes, B.; Pohl, T.M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66685

A:Accession: S67074

A:Molecule type: DNA

A:Residues: 1-63 <HUG>

A:Cross-references: EMBL:Z75090; GSPDB:GN00015; MIPS:YOR182c; NID:g1420438; PIDN:CAA

A:Experimental source: strain S288C

A:Genetics: YS30B

R:Baker, R.T.; Williamson, N.A.; Wettenhall, R.E.H.

J. Biol. Chem. 271, 13549-13555, 1996

A:Title: The yeast homolog of mammalian ribosomal protein S30 is expressed from a du

A:Reference number: S70774; MUID:96278780; PMID:8662789

A:Accession: S70775

A:Molecule type: DNA

A:Residues: 1-63 <BAK>

A:Cross-references: EMBL:U48700; NID:g1256752; PIDN:AAC49316.1; PID:g1256753

A:Genetics: YS30A

A:Accession: S70776

A:Molecule type: mRNA

A:Residues: 1-63 <BAV>

A:Cross-references: EMBL:U48699; NID:g1256750; PIDN:AAC49316.1; PID:g1256751

A:Genetics: YS30A

A:Accession: S70774

A:Molecule type: protein

A:Residues: 2-63 <BA3>

C:Genetics: <YS30B>

A:Gene: SCD:RPS30B; MIPS:YOR182c

A:Cross-references: MIPS:YOR182c; SGD:S0005708
 A:Map position: 15R
 A:introns: 1/3
 C:Genetics: <YS30A>
 A:Gene: SGD-RPS30A; MIPS:YLR287c-a
 A:Cross-references: MIPS:YLR287c-a; SGD:S0004278
 A:Map position: 12R
 A:introns: 1/3
 C:Superfamily: yeast ribosomal protein S30.e
 C:Keywords: cytosol; protein biosynthesis; ribosome
 F:2-63/Product: ribosomal protein S30.e, cytosolic #status experimental <MAT>

Query Match 20.3%; Score 12; DB 1; Length 63;
 Best Local Similarity 100.0%; Pred. No. 4.9e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVHGLARAGKY 12
 |||||
 DB 3 KVHGLARAGKY 14

RESULT 11

A97094
 uncharacterized protein, YDF B. subtilis ortholog [Imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: A97094
 R:Noilling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Bacteriol. 183; 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: A97094
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-135 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK79540.1; PID:G15024526; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC1573

Query Match 13.6%; Score 8; DB 2; Length 135;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 KOEKKKKK 28
 |||||
 DB 124 KOEKKKKK 131

RESULT 12

S02776
 DNA-binding protein H-NS - Proteus vulgaris
 C:Species: Proteus vulgaris
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 13-Sep-1998
 C:Accession: S02776
 R:la Teana, A.; Falconi, M.; Scarlato, V.; Iammi, M.; Pon, C.L.
 FEBS Lett. 244, 34-38, 1989
 A:Title: Characterization of the structural genes for the DNA-binding protein H-NS in E.
 A:Reference number: S02775; MUID:89171270; PMID:2494066
 A:Accession: S02776
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-134 <LAL>
 C:Genetics:
 A:Gene: hns
 C:Function:
 A:Description: binds double-stranded DNA; influences regulation of gene expression at tr
 C:Superfamily: DNA-binding protein H-NS
 C:Keywords: DNA binding; transcription regulation

Query Match 11.9%; Score 7; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 9.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 28 KTRAKR 34
 |||||
 DB 83 KTRAKR 89

RESULT 13

B75305
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: B75305
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: B75305
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-154 <WHI>
 A:Cross-references: GB:AE002051; GB:AE000513; NID:96459976; PIDN:AAF11732.1; PID:964
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2179
 A:Map position: 1

Query Match 11.9%; Score 7; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 RAGKVRG 14
 |||||
 DB 39 RAGKVRG 45

RESULT 14

E84782
 probable homeodomain transcription factor [Imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: E84782
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VarAken, S.E.; Umayam, L.; Tallon,
 euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84782
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-199 <STO>
 A:Cross-references: GB:AE002093; NID:94415906; PIDN:AAD20137.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: AT2G36610
 A:Map position: 2

Query Match 11.9%; Score 7; DB 2; Length 199;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 QEKKKKK 28
 |||||
 DB 68 QEKKKKK 74

RESULT 15

I52523
 nucleoporin p62 homolog - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 05-Nov-1999

C:Accession: I52523
 R:Wang, Z.Q.; Akmal, K.M.; Kim, K.H.
 Biol. Reprod. 51, 1022-1030, 1994
 A:Title: An unusual nucleoprotein-related messenger ribonucleic acid is present in the ger
 A:Reference number: I52523; MUID:95151924; PMID:7849178
 A:Accession: I52523
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-215 <RES>
 A:Cross-references: GB:S75997; NID:9913245; PIDN:AA93384.1; PID:9913246
 A:Experimental source: testis

Query Match 11.9%; Score 7; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 EKKKKTG 30
 |||||
 DB 52 KKKKKTG 58

RESULT 16
 H86318
 Probable 60S ribosomal protein L6 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H86318
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Ansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 A:Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: AB6141; MUID:21016719; PMID:11130712
 A:Accession: H86318
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <STO>
 A:Cross-references: GB:AE005172; NID:9795602; PIDN:AA98420.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 11.9%; Score 7; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKT 29
 |||||
 DB 166 EKKKKT 172

RESULT 17
 D96768
 Protein 60S ribosomal protein L6 P2P9.8 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: D96768
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Ansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 A:Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: AB6141; MUID:21016719; PMID:11130712
 A:Accession: D96768

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <STO>
 A:Cross-references: GB:AE005173; NID:97109467; PIDN:AA936731.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F2P9.8
 A:Map position: 1

Query Match 11.9%; Score 7; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKT 29
 |||||
 DB 166 EKKKKT 172

RESULT 18
 E96768
 Protein 60S ribosomal protein L6 P2P9.7 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: E96768
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 Ansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim
 A:Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: AB6141; MUID:21016719; PMID:11130712
 A:Accession: E96768
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <STO>
 A:Cross-references: GB:AE005173; NID:97109466; PIDN:AA936730.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F2P9.7
 A:Map position: 1

Query Match 11.9%; Score 7; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKT 29
 |||||
 DB 166 EKKKKT 172

RESULT 19
 T47174
 Hypothetical protein DKFZp7621166.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
 C:Accession: T47174
 R:Blocker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Well, B.; Wiemann, S.
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: 224376
 A:Accession: T47174
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-283 <AAA>
 A:Cross-references: EMBL:AL162072
 A:Experimental source: adult melanoma (Mewo cell line); clone DKFZp7621166
 C:Genetics:
 A:Note: DKFZp7621166.1
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology
 Query Match 11.9%; Score 7; DB 2; Length 283;
 Best Local Similarity 100.0%; Pred. No. 18;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GSLARAG 10
|||||||
Db 236 GSLARAG 242

RESULT 20

D70313

riboflavin kinase - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Sep-1999

C:Accession: D70313

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

V.

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: D70313

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-314 <AQF>

A:Cross-references: GB:AE000675; NID:g2982863; PIDN:AC06488.1; PID:g2982868; GB:AE00065

A:Experimental source: strain VF5

C:Genetics:

A:Gene: ribF

C:Superfamily: conserved hypothetical protein H10963

Query Match 11.9%; Score 7; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 47 PTFGRKK 53
|||||||
Db 253 PTFGRKK 259

RESULT 21

T19629

hypothetical protein C32A3.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19629

R:Thomas, K.

submitted to the EMBL Data Library, February 1995

A:Reference number: Z19154

A:Accession: T19629

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-346 <WIL>

A:Cross-references: EMBL:Z48241; PIDN:CAA8285.1; GSPDB:GN00021; CESP:C32A3.2

A:Experimental source: clone C32A3

C:Genetics:

A:Gene: CESP:C32A3.2

A:Map position: 3

A:Introns: 47/3; 79/3; 111/2; 165/2; 266/1

Query Match 11.9%; Score 7; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 23 EKKRKKKT 29
|||||||
Db 6 EKKRKKKT 12

RESULT 22

T36154

Probable ABC-type transport system ATP-binding protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T36154

R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, July 1999

A:Reference number: Z21598

A:Accession: T36154

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-424 <SEB>

A:Cross-references: EMBL:AL096852; PIDN:CAB51012.1; GSPDB:GN00070; SCOEDB:SCE19A.31

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCE19A.31

Query Match 11.9%; Score 7; DB 2; Length 424;
Best Local Similarity 100.0%; Pred. No. 25;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GSLARAG 10
|||||||
Db 328 GSLARAG 334

RESULT 23

E84153

replicative DNA helicase dnaC [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: E84153

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;

Nucleic Acids Res. 28: 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: E84153

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-454 <STO>

A:Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BA07748.1; GSPDB:

A:Experimental source: strain C-125

C:Genetics:

A:Gene: dnaC

C:Superfamily: phage P22 gene 12 protein

Query Match 11.9%; Score 7; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GSLARAG 10
|||||||
Db 281 GSLARAG 287

RESULT 24

T49516

Atu related protein [imported] - Neurospora crassa

N:Alternate names: protein B14D6.680

C:Species: Neurospora crassa

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T49516

R:Schulte, U.; Algn, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakati

submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25022

A:Accession: T49516

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-710 <SCH>

A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.680

A:Experimental source: BAC clone B14D6; strain OR74A

C:Genetics:

A:Gene: NCSP:B14D6.680

A:Map position: 6

A:Introns: 422/1

Query Match 11.9%; Score 7; DB 2; Length 710;
Best Local Similarity 100.0%; Pred. No. 39;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 QEKKKKK 28
|||||||
Db 700 QEKKKKK 706

RESULT 25

F85343
hypothetical protein AT4g29450 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C:Accession: F85343
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: AB5001; MUID:20083488; PMID:10617198
A:Accession: F85343
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-863 <STO>
A:Cross-references: GB:NC_001268; NID:g7269844; PIDN:CAB79703.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g29450
A:Map position: 4
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 11.9%; Score 7; DB 2; Length 863;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 QEKKKKK 28
|||||||
Db 504 QEKKKKK 510

RESULT 26

J01979
structural polypeptide - Venezuelan equine encephalitis virus (subtype I, strain Menatt)
N:Contains: 6K protein; coat protein; membrane glycoprotein E1; membrane glycoprotein E2
C:Species: Venezuelan equine encephalitis virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C:Accession: J01979
R:Neider, J.M.; Kinney, R.M.; Tsuchiya, K.R.; Trent, D.W.
J. Gen. Virol. 74, 519-523, 1993
A:title: Molecular evidence that epizootic Venezuelan equine encephalitis (VEE) I-AB vir
A:Reference number: J01978; MUID:93187617; PMID:8445371
A:Accession: J01979
A:Molecule type: mRNA
A:Residues: 1-1254 <SNE>
A:Cross-references: GB:I04599; NID:g290619; PIDN:AAA2990.1; PID:g290621
C:Superfamily: togavirus structural polypeptide
C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-274/Product: coat protein #status predicted <CTP>
F:275-333/Product: membrane glycoprotein E1 #status predicted <MG3>
F:334-756/Product: membrane glycoprotein E2 #status predicted <MG2>
F:701-721/Product: transmembrane #status predicted <TM1>
F:757-812/Product: 6K protein #status predicted <KP6>
F:94-813/Domain: transmembrane #status predicted <TM2>
F:813-1254/Product: membrane glycoprotein E1 #status predicted <MG1>
F:1231-1248/Domain: transmembrane #status predicted <TM3>
F:47,285,651,946/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.9%; Score 7; DB 1; Length 1254;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 KKKKKTG 30
|||||||
Db 88 KKKKKTG 94

RESULT 27

B71619

hypothetical protein PFB0280w - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: B71619
R:Gardner, M.J.; Tetteijn, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
; Pereira, M.; Salzberg, S.; Zhou, L.; Sutton, G.C.; Clayton, R.; White, O.; Smith, H
Science 282, 1126-1132, 1998
A:title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9604551
A:Accession: B71619
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-2539 <GAR>
A:Cross-references: GB:AE001384; GB:AE001362; NID:g3845139; PIDN:AACT1845.1; PID:g384
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0280w

Query Match 11.9%; Score 7; DB 2; Length 2539;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 QEKKKKK 28
|||||||
Db 692 QEKKKKK 698

RESULT 28

T28799
hypothetical protein C16E9.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T28799
R:Giesel, C.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C16E9.
A:Reference number: Z20525
A:Accession: T28799
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-46 <GEI>
A:Cross-references: EMBL:U039677; PIDN:AACT47959.1; GSPDB:GN00028; CESP:C16E9.5
C:Experimental source: strain Bristol N2; clone C16E9
C:Genetics:
A:Gene: CESP:C16E9.5
A:Map position: X

Query Match 10.2%; Score 6; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKK 28
|||||||
Db 2 EKKKKK 7

RESULT 29

B69830
hypothetical protein ynfD - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: B69830
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Enlilich, S.D.; Emerson, P.T.; Eutlian, K.D.; Erlington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fume, S.; Gallizzi, A.; Gall
tech, J.; Harwood, C.R.; Henault, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Huilo, T
Koelter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, A.; Lapidus, A.; Lardino
A.; Others: Leuber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portet
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: B69830
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-67 <KUN>
 A:Cross-references: GB:Z99109; GB:AL009126; NID:q2633260; PIDN:CAB12859.1; PID:e1183021;
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: ynfD

Query Match 10.2%; Score 6; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 EKKKK 28
 Db 46 EKKKK 51

RESULT 30
 H97135
 uncharacterized phage related protein [Imported] - *Clostridium acetobutylicum*
 C:Species: *Clostridium acetobutylicum*
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: H97135
 R:Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: H97135
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-70 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK79875.1; PID:q15024892; GSPDB:GN00168
 A:Experimental source: *Clostridium acetobutylicum* ATCC824
 C:Genetics:
 A:Gene: CAC1912

Query Match 10.2%; Score 6; DB 2; Length 70;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 TGRKR 34
 Db 19 TGRKR 24

RESULT 31
 T47434
 hypothetical protein T22K7.120 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T47434
 R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: 224459
 A:Accession: T47434
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-74 <RIE>
 A:Cross-references: EMBL:AL138641
 A:Experimental source: cultivar Columbia; BAC clone T22K7
 C:Genetics:
 A:Map position: 3
 A:Introns: 31/3
 A:Note: T22K7.120

Query Match 10.2%; Score 6; DB 2; Length 74;

Best Local Similarity 100.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 KKKKK 29
 Db 69 KKKKK 74

RESULT 32
 B82267
 exodeoxyribonuclease, small chain VC0891 [Imported] - *Vibrio cholerae* (strain N16961)
 C:Species: *Vibrio cholerae*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: B82267
 R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.; Chardson, D.; Ermolaeva, M.D.; Yamatyan, J.; Basa, S.; Qin, H.; Dragol, I.; Sellers, L.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: B82267
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-80 <HEI>
 A:Cross-references: GB:AE004173; GB:AE003852; NID:q9655341; PIDN:AAF94053.1; GSPDB:GN
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC0891
 A:Map position: 1
 C:Superfamily: exodeoxyribonuclease VII small chain

Query Match 10.2%; Score 6; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 SLARAG 10
 Db 44 SLARAG 49

RESULT 33
 S66013
 ribosomal protein S18 (rpsr) - *Bacillus subtilis*
 N:Alternate names: ribosomal protein BS21
 C:Species: *Bacillus subtilis*
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
 C:Accession: S66013; S11368; A69701
 R:Ogasawara, N.; Nakai, S.; Yoshikawa, H.
 DNA Res. 1, 1-14, 1994
 A:Title: Systematic sequencing of the 180 kilobase region of the *Bacillus subtilis* ch
 A:Reference number: S65967; MUID:96051385; PMID:7584024
 A:Accession: S66013
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-81 <OGA>
 A:Cross-references: EMBL:D26185; NID:q467326; PIDN:BA05219.1; PID:q467373
 A:Experimental source: strain 168
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
 M:Hiso, K.I.; Otake, E.; Osawa, S.
 Mol. Gen. Genet. 185, 239-244, 1982
 A:Title: Purification and characterization of 30S ribosomal proteins from *Bacillus su*
 A:Reference number: S09561; MUID:82219212; PMID:6806564
 A:Accession: S11368
 A:Molecule type: protein
 A:Residues: 4-26 <HIG>
 A:Experimental source: strain 168
 A:Note: 20-ASP was also found
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.;
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gal
 tech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M

Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, akuch, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Milters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A. A.; Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*. A; Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: A69701

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-81 <RND>

A;Cross-references: GB:299124; GB:AL009126; NID:92636442; PIDN:CAB16126.1; PID:92636636

A;Experimental source: strain 168

C;Genetics:

A;Gene: rpsR

C;Superfamily: Escherichia coli ribosomal protein S18

C;Keywords: acetylated amino end; protein biosynthesis; ribosome

F;4-81/Product: ribosomal protein S18 #status experimental <MAT>

F;4/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

Query Match 10.2%; Score 6; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 30 GRAKRR 35
|||||
Db 10 GRAKRR 15

RESULT 34

T36134

hypothetical protein SCE19A.11c - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-Jan-2001

C;Accession: T36134

R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999

A;Reference number: Z21598

A;Accession: T36134

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-92 <SEF>

A;Cross-references: EMBL:AL096852; PIDN:CAB50992.1; GSPDB:GN00070; SCOEDB:SCE19A.11c

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOEDB:SCE19A.11c

C;Superfamily: probable sulfur carrier protein slr0821

Query Match 10.2%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 40 RRFYNV 45
|||||
Db 53 RRFYNV 58

RESULT 35

H82867

transcription regulator xFa0057 [imported] - *Xylella fastidiosa* (strain 9a5c)

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

C;Accession: H82867

R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A;Reference number: A82515; MUID:20355717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: H82867

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-92 <STM>

A;Cross-references: GB:AE003851; NID:99112238; PIDN:AAF85625.1; GSPDB:GN00130; XFSC:}

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. B;Riones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrei as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to Genbank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Pi J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Le chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savi A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv M.; Tshahro, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovsky-Almeida, S.; Vettore, A.L. A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: xFa0057

A;Genome: plasmid

A;Note: plasmid pXF5.1

Query Match 10.2%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 31 RAKRRM 36
|||||
Db 12 RAKRRM 17

RESULT 36

H96585

hypothetical protein F20D21.23 [imported] - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cross)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C;Accession: H96585

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hultzar, L. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Maritz Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shim, P.; Southwick, A.M.; Sun, H.; Talic ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*. A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: H96585

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-98 <STO>

A;Cross-references: GB:AE005173; NID:94585983; PIDN:AAD25619.1; GSPDB:GN00141

C;Genetics:

A;Gene: F20D21.23

A;Map position: 1

Query Match 10.2%; Score 6; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 23 EKRRKK 28
|||||
Db 71 EKRRKK 76

RESULT 37

T07078

cold stress protein SRC1 - soybean

C;Species: Glycine max (soybean)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000

C;Accession: T07078

R.Takahashi, R.; Shimosaka, E.

Plant. Sci. 123, 93-104, 1997

A>Title: CDNA sequence analysis and expression of two cold-regulated genes in soybean.

A:Reference number: Z15902

A:Accession: T07078

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-102 <YAK>

A:Cross-references: EMBL:AB000129; PIDN:BAA19768.1

A:Experimental source: cultivar Kitamumume

C:Genetics:

A:Gene: srcl

C:Superfamily: cold stress protein COR19

C:Keywords: cold shock

Query Match

Best Local Similarity 100.0%; Score 6; DB 2; Length 102;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28

DB 76 EKKKKK 81

RESULT 38

C87604

virulence-associated protein, probable [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: C87604

R:Neeman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A>Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:1125647

A:Accession: C87604

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-104 <STO>

A:Cross-references: GB:AE005673; NID:q13424481; PIDN:AAK24831.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2867

Query Match

Best Local Similarity 100.0%; Score 6; DB 2; Length 104;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 VRGQTP 17

DB 51 VRGQTP 56

RESULT 39

PM0017

hypothetical protein 105 (gsm 3' region) - Micromonospora purpurea (fragment)

C:Species: Micromonospora purpurea

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994

C:Accession: PM0017

R:Kleimen, G.H.; Cundliffe, E.; Financsek, I.

Gene 98, 53-60, 1991

A>Title: Cloning and characterization of gentamicin-resistance genes from Micromonospora

A:Reference number: JG0017; MUID:91192615; PMID:2013410

A:Accession: PM0017

A:Molecule type: DNA

A:Residues: 1-105 <KEU>

A:Cross-references: GB:M55520

A>Note: the authors translated the codon CCG for residues 27, 30, 31, and 37 as Phe and

C:Keywords: antibiotic resistance

Query Match

Best Local Similarity 100.0%; Score 6; DB 2; Length 105;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 10

DB 11 SLARAG 16

RESULT 40

PM0018

hypothetical protein 105 - Micromonospora sp. (fragment)

C:Species: Micromonospora sp.

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994

C:Accession: PM0018

R:Kleimen, G.H.; Cundliffe, E.; Financsek, I.

Gene 98, 53-60, 1991

A>Title: Cloning and characterization of gentamicin-resistance genes from Micromonospora

A:Reference number: JG0017; MUID:91192615; PMID:2013410

A:Accession: PM0018

A:Molecule type: DNA

A:Residues: 1-105 <KEU>

A:Cross-references: GB:M55521

A>Note: the authors translated the codon CCG for residues 27, 30, 31, and 37 as Phe and

Query Match

Best Local Similarity 100.0%; Score 6; DB 2; Length 105;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 10

DB 11 SLARAG 16

RESULT 41

S59536

cold stress protein COR1 - Poncirus trifoliata

C:Species: Poncirus trifoliata

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Sep-1999

C:Accession: S59536

R:Cal, O.; Moore, G.A.; Guy, C.L.

Plant Mol. Biol. 29, 11-23, 1995

A>Title: An unusual group 2 LEA gene family in citrus responsive to low temperature.

A:Reference number: S59534; MUID:96017610; PMID:7579157

A:Accession: S59536

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-106 <CAI>

A:Cross-references: EMBL:L39005; NID:9625154; PIDN:AAA99963.1; PID:9625155

A:Experimental source: seedling; tissue type leaf

C:Superfamily: cold stress protein COR19

C:Keywords: cold shock

Query Match

Best Local Similarity 100.0%; Score 6; DB 2; Length 106;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28

DB 87 EKKKKK 92

RESULT 42

S69849

hypothetical protein YMR290w-a - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 26-Aug-1999

C:Accession: S69849

R:Barrell, B.G.

submitted to the EMBL Data Library, August 1994

A:Reference number: S47445

A:Accession: S69849

A:Molecule type: DNA

A:Residues: 1-115 <BAR>

A:Cross-references: EMBL:X80836; MIPS:YMR290w-a

C:Genetics:

A:Map position: 13R
C:Superfamily: Saccharomyces hypothetical protein YMR290W-a

Query Match 10.2%; Score 6; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||
DB 98 EKKKK 103

RESULT 43

H84651
hypothetical protein Atg25720 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84651
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84651
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <STO>
A:Cross-references: GB:AE002093; NID:g4874310; PIDN:AAD31372.1; GSPDB:GN00139
C:Genetics:
A:Gene: Atg25720
A:Map position: 2

Query Match 10.2%; Score 6; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||
DB 27 EKKKK 32

RESULT 44

B71268
probable ribosomal protein L19 (rplS) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 13-Aug-1999
C:Accession: B71268
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; MCD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A>Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:965876
A:Accession: B71268
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-123 <COL>
A:Cross-references: GB:AE001259; GB:AE00520; NID:g3323209; PIDN:AAC65861.1; PID:g332322
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0909
C:Superfamily: Escherichia coli ribosomal protein L19

Query Match 10.2%; Score 6; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 RAGKV 13
|||||
DB 89 RAGKV 94

RESULT 45

R3R725
ribosomal protein S25, cytosolic [validated] - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jul-2000
C:Accession: A38969; S17353
R:Chan, Y.L.; Wool, I.G.
Biochem. Biophys. Res. Commun. 186, 1688-1693, 1992
A>Title: The primary structure of rat ribosomal protein S25.
A:Reference number: JH0691; MUID:92378645; PMID:1354961
A:Accession: A38969
A:Molecule type: mRNA
A:Residues: 1-125 <CH2>
A:Cross-references: EMBL:X62482; NID:957723; PIDN:CAA44349.1; PID:957724
A>Note: the protein is designated as ribosomal protein S25 by comparison to the comp
C:Superfamily: rat ribosomal protein S25
C:Keywords: protein biosynthesis; ribosome

Query Match 10.2%; Score 6; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSLAR 9
|||||
DB 81 GSLAR 86

Search completed: February 6, 2003, 21:32:13
Job time : 21 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 21:29:24 : Search time 29 Seconds
(without alignments)
419.199 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59
Sequence: 1 KVHGLARAGKVRGQPRKVA.....RRFVNVVPTFGKKKGPANNS 59

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	133	4 Q9H5V4	Q9H5V4 homo sapien
2	59	100.0	133	11 Q9J324	Q9J324 mus musculu
3	59	100.0	137	11 Q920W8	Q920W8 mus musculu
4	59	100.0	137	11 Q920W7	Q920W7 mus splicile
5	59	100.0	137	11 Q91V99	Q91V99 mus musculu
6	23	39.0	133	13 Q90YPI	Q90YPI ictalurus p
7	22	37.3	62	10 Q9MDE4	Q9MDE4 arabidopsis
8	21	35.6	230	4 Q15351	Q15351 homo sapien
9	15	25.4	132	5 Q9VDH8	Q9VDH8 drosophila
10	13	22.0	130	5 Q18231	Q18231 caenorhabdi
11	12	20.3	131	5 Q962G1	Q962G1 spodoptera
12	9	15.3	309	10 Q9S3U0	Q9S3U0 arabidopsis
13	8	13.6	135	16 Q971R7	Q971R7 clostridium
14	7	11.9	134	2 Q9L657	Q9L657 proteus mir
15	7	11.9	154	16 Q9RSE5	Q9RSE5 delnoccocus
16	7	11.9	157	5 Q9NBB4	Q9NBB4 drosophila

17	7	11.9	173	10 Q9ZOB1	Q9ZOB1 arabidopsis
18	7	11.9	198	2 Q9ACU8	Q9ACU8 bruceella ab
19	7	11.9	215	11 Q64075	Q64075 rattus sp.
20	7	11.9	224	10 Q9L1R5	Q9L1R5 arabidopsis
21	7	11.9	233	10 Q9F276	Q9F276 arabidopsis
22	7	11.9	233	10 Q9C9C6	Q9C9C6 arabidopsis
23	7	11.9	233	10 Q9C9C5	Q9C9C5 arabidopsis
24	7	11.9	259	16 Q9AD23	Q9AD23 streptomyc
25	7	11.9	283	4 Q9NSK3	Q9NSK3 homo sapien
26	7	11.9	309	5 Q95T41	Q95T41 drosophila
27	7	11.9	314	16 Q66535	Q66535 aquifex aeo
28	7	11.9	339	5 Q95XC7	Q95XC7 caenorhabdi
29	7	11.9	380	4 Q96GN4	Q96GN4 homo sapien
30	7	11.9	380	5 Q9W0W6	Q9W0W6 drosophila
31	7	11.9	381	4 Q15694	Q15694 homo sapien
32	7	11.9	424	16 Q9S2F0	Q9S2F0 streptomyc
33	7	11.9	429	2 Q9X4J1	Q9X4J1 streptomyc
34	7	11.9	454	16 Q9K5Q9	Q9K5Q9 bacillus ha
35	7	11.9	542	13 Q91290	Q91290 pleurodeles
36	7	11.9	575	4 Q9NXU4	Q9NXU4 homo sapien
37	7	11.9	594	16 Q98CL9	Q98CL9 thizobium l
38	7	11.9	806	10 Q9M8T5	Q9M8T5 arabidopsis
39	7	11.9	863	10 Q9M0D8	Q9M0D8 arabidopsis
40	7	11.9	1254	12 Q9WC26	Q9WC26 venezuelan
41	7	11.9	1254	12 Q9YKD3	Q9YKD3 venezuelan
42	7	11.9	1254	12 Q88979	Q88979 venezuelan
43	7	11.9	1254	12 Q8V293	Q8V293 venezuelan
44	7	11.9	1254	12 Q8V291	Q8V291 venezuelan
45	7	11.9	1264	12 Q8UYH1	Q8UYH1 venezuelan

ALIGNMENTS

RESULT 1

Q9H5V4 PRELIMINARY; PRT; 133 AA.

ID Q9H5V4
AC Q9H5V4:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA: FLJ22986 f1s, clone KAT11742.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe K., Kunagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohayashi M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isegaki T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK026639; BAB15515.1; -.
DR HSSP: P02248; IUBI.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; Ubiquitin.1.
DR PRINTS: PR00348; Ubiquitin.
DR SMART: SM00213; UBO.1.
DR PROSITE: PS00299; Ubiquitin.1; 1.
DR PROSITE: PS50053; Ubiquitin.2; 1.
SQ SEQUENCE 133 AA; 14390 MW; 5D2F81F2A355B559 CMC64;

Query Match 100.0%; Score 59; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.5e-56;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHGLARAGKVRGQPRKVAQEKKKKTGAKRMOYNRRFVNVVPTFGKKKGPANNS 59
Db 75 KVHGLARAGKVRGQTPVAAQEKKKKTGAKRMOYNRRFVNVVPTFGKKKGPANNS 133
RESULT 2

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09J324
ID 09J324 PRELIMINARY: PRT: 133 AA.
AC 09J324:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Monoclonal non-specific suppressor factor beta (Finkel-Biskis-Reilly
DE murine Sarcoma virus (FSR-MuSV) ubiquitously expressed) (fox
DE derived).
GN FAU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS OB;
RA Nie G.-Y., Li Y., Salomonsen L.A., Clements J.A., Findlay J.K.;
RT "Identification of monoclonal non-specific suppressor factor beta as
RT one of the genes differentially expressed at implantation sites
RT compared to interimplantation sites in the mouse uterus.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE, AND KIDNEY;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AF147745; AAF80246.1; -
DR EMBL: AK008466; BAB25684.1; -
DR EMBL: AK002355; BAB22034.1; -
DR HSSP: P02248; IUBT.
DR MGD: MGI:102347; Fau.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin.1.
DR PRINTS: PR00348; UBIOUITIN.
DR SMART: SM00213; UBO.1.
DR PROSITE: PS00299; UBIOUITIN_1; 1.
DR PROSITE: PS50053; UBIOUITIN_2; 1.
SQ SEQUENCE 133 AA; 14416 MW; 2087C774A022AB16 CRC64;

Query Match 100.0%; Score 59; DB 11; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.5e-56;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPVANS 59
Db 75 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPVANS 133

RESULT 3
O920W8 PRELIMINARY: PRT: 137 AA.
AC 0920W8:
DT 01-DEC-2001 (TREMBLrel. 19, Created)

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DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Fcu protein (Fragment).
GN FAU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BLG2/MSF;
RA Liu Y., Kitano T., Koide T., Shirosaki T., Moriwaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB039086; BAB68610.1; -
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin.1.
DR PROSITE: PS00299; UBIOUITIN_1; UNKNOWN_1.
DR PROSITE: PS50053; UBIOUITIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 137 AA; 14845 MW; 57099FF405D8B2B CRC64;

Query Match 100.0%; Score 59; DB 11; Length 137;
Best Local Similarity 100.0%; Pred. No. 3.6e-56;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPVANS 59
Db 79 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPVANS 137

RESULT 4
O920W7 PRELIMINARY: PRT: 137 AA.
AC 0920W7:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Fcu protein (Fragment).
GN FAU.
OS Mus spicilegus (Steppe mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZBN;
RA Liu Y., Kitano T., Koide T., Shirosaki T., Moriwaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB039093; BAB68617.1; -
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin.1.
DR PROSITE: PS00299; UBIOUITIN_1; UNKNOWN_1.
DR PROSITE: PS50053; UBIOUITIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 137 AA; 14787 MW; 57099FF7065D8828 CRC64;

Query Match 100.0%; Score 59; DB 11; Length 137;
Best Local Similarity 100.0%; Pred. No. 3.6e-56;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPVANS 59
Db 79 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPVANS 137

RESULT 5
O91V99 PRELIMINARY: PRT: 137 AA.
AC 091V99:
DT 01-DEC-2001 (TREMBLrel. 19, Created)

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DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Fau protein (Fragment).
OS
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIABLE STRAINS:
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
RT "Conspicuous differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039084; BAB68608.1; -;
DR EMBL; AB039085; BAB68609.1; -;
DR EMBL; AB039087; BAB68611.1; -;
DR EMBL; AB039088; BAB68612.1; -;
DR EMBL; AB039089; BAB68613.1; -;
DR EMBL; AB039090; BAB68614.1; -;
DR EMBL; AB039091; BAB68615.1; -;
DR EMBL; AB039092; BAB68616.1; -;
DR InterPro: IPR000626; Ubligutlin.
DR Pfam: PF00240; Ubligutlin.1.
DR PROSITE: PS00299; UBIQUITIN_1; UNKNOWN_1.
DR PROSITE: PS0053; UBIQUITIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 137 AA; 14787 MW; 57099FF7065D8828 CRC64;

Query Match 100.0%; Score 59; DB 11; Length 137;
Best Local Similarity 100.0%; Pred. No. 3.6e-56;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KHVHSLARACKVRCQTPKVAKEKKKKTKGRKRMQYNRFVNVVPTFGKKKGNPANS 59
Db 79 KHVHSLARACKVRCQTPKVAKEKKKKTKGRKRMQYNRFVNVVPTFGKKKGNPANS 137

RESULT 6
Q90YPI PRELIMINARY; PRT; 133 AA.
AC Q90YPI;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE 40S ribosomal protein S30.
OS Ictulurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Karsl A., Patterson A., Feng J., Liu Z.J.;
RT "Translational machinery of channel catfish: I. A transcriptomic
RT approach to the analysis of 32 40S ribosomal protein genes and their
RT expression.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF02841; AAR95215.1; -;
DR InterPro: IPR000626; Ubligutlin.
DR Pfam: PF00240; Ubligutlin.1.
DR PROSITE: PS0053; UBIQUITIN_2; 1.
KW Ribosomal protein.
SQ SEQUENCE 133 AA; 14504 MW; 62036BB0E72C5CAC CRC64;

Query Match 39.0%; Score 23; DB 13; Length 133;
Best Local Similarity 100.0%; Pred. No. 4.1e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 QYNRRFVNVVPTFGKKKGNPANS 59
|||||

Db 111 QYNRRFVNVVPTFGKKKGNPANS 133

RESULT 7
ID Q9MOE4 PRELIMINARY; PRT; 62 AA.
AC Q9MOE4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Ribosomal protein S30 homolog (40S ribosomal protein S30 homolog)
DE (At2g19750/F6F22.22).
DE ATG29390.
GN Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyaajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Sequence features of the regions of 1,367,185 bp covered by 19
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:203-216(1998).
RN [4]
RP SEQUENCE FROM N.A.
RA Shin P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL161574; CAB79697.1; -;
DR EMBL; AB013392; BAB09885.1; -;
DR EMBL; AY052341; AAR95533.1; -;
DR EMBL; AY061910; AAL31237.1; -;
KW Ribosomal protein.
SQ SEQUENCE 62 AA; 6887 MW; 95D8F3B72F53F33 CRC64;

Query Match 37.38%; Score 22; DB 10; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KHVHSLARACKVRCQTPKVAKQ 22

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Db      3 KVGSLARAGKVGOTPKVAKO 24
|||||
RESULT 8
ID      015351      PRELIMINARY;      PRT;      230 AA.
AC      015351;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
SEB4B (Fragment).
GN      SEB4B(HUMAN).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;

RP      SEQUENCE FROM N.A.
RC      TISSUE=THYMUS;
RA      Ruehlmann A., Gupta A., Terhorst C.;
RT      "A novel murine RRM-type protein and its human homolog.";
RL      Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR      EMBL: X75315; CA53064.1; -.
DR      HSP: P09651; IUP1.
DR      InterPro: IPR000504; RNA_rec_mot.
DR      Pfam: PF00076; rrm; 1.
DR      SMART: SMO0360; RRM; 1.
DR      PROSITE: PS0102; RRM; 1.
DR      PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
FT      NON_TER
SQ      SEQUENCE 230 AA; 25220 MW; C747D6500608461 CRC64;

Query Match      35.6%; Score 21; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      34 RRMQYRRFVNVVPTFGKKKG 54
Db      1 RRMQYRRFVNVVPTFGKKKG 21
|||||

RESULT 9
ID      09VDH8      PRELIMINARY;      PRT;      132 AA.
AC      09VDH8;
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE      CG15697 protein (RH08962p).
GN      CG15697.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BERKELEY;
RX      MEDLINE=20196006; PubMed-10731132;
RA      Adams M.D., Ceinliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA      Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA      George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA      Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA      Brandon R.C., Rogers Y.H.C., Blazej R.G., Champs M., Felhofer B.D.,
RA      Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA      Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA      Ballew R.M., Basu A., Baxendale J., Bayraktiroglu L., Beasley E.M.,
RA      Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA      Borovna D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
RA      Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA      Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA      de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA      Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA      Durbin K.J., Evangelista C.C., Feriaz C., Ferriere S., Fleischmann W.,
RA      Foster C., Gabriellian A.E., Garg N.S., Gelbart W.N., Glasser K.,
RA      Glodek A., Gong F., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA      Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
RA      Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
RA      Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA      Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA      Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA      Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA      Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA      Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA      Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA      Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA      Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA      Shue B.C., Sidden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA      Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA      Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA      Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA      Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA      Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA      Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA      Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT      "The genome sequence of Drosophila melanogaster.";
RL      Science 287:2185-2195(2000).

RP      SEQUENCE FROM N.A.
RC      STRAIN=BERKELEY;
RA      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA      Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fise E.,
RA      George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA      Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
RA      Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA      Ceinliker S.;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AEO03732; AAF55815.1; -.
DR      FLYBASE: FBgn0038834; CG15697.
DR      InterPro: IPR000626; Ubiqultin.
DR      Pfam: PF00240; ubiqlutin; 1.
SQ      SEQUENCE 132 AA; 14585 MW; E07C54F316FD5 CRC64;

Query Match      25.4%; Score 15; DB 5; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 KOEKKKKKTGRARR 35
Db      93 KOEKKKKKTGRARR 107
|||||

RESULT 10
ID      018231      PRELIMINARY;      PRT;      130 AA.
AC      018231;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE      C26F1.4 protein.
GN      C26F1.4.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BRISTOL N2;
RX      MEDLINE=94150718; PubMed-7906398;
RA      Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA      Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA      Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA      Garner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA      Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

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RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Smailson N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Tilleray-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Wooldman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Geisel C., Stellyes L., Bradshaw H.;
 RT "The sequence of C. elegans cosmid C26F1.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U53148; AAB37076.1; -.
 DR HSSP; P02248; IUBI.
 DR InterPro: IPR000626; Ubiqutin.
 DR Pfam: PF00240; ubiqutin; 1.
 DR SMART: SM00213; UBO; 1.
 SQ SEQUENCE 130 AA; 14033 MW; 50DC09AFB9F48532 CRC64;
 Query Match 22.0%; Score 13; DB 5; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.9e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVHSLARACKV 13
 DB 72 KVHSLARACKV 84

RESULT 11
 096201 PRELIMINARY; PRT; 131 AA.
 AC 096201;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Ribosomal protein S30.
 OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuidae; Noctuidae; Amphipyritinae; Spodoptera.
 OX NCBI_TaxID=7108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Landels I., Ogilastro M., Mita K., Nohata J., Lopez-Ferber M.,
 RA Donot-Cerutti M., Fournier P., Devauchelle G.;
 RT "Full-length ribosomal protein sequence from an EST library of
 RT Spodoptera frugiperda cells (Sf9).";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF400225; AAK92197.1; -.
 SQ SEQUENCE 131 AA; 14314 MW; 03AE0E31EB1B04 CRC64;
 Query Match 20.3%; Score 12; DB 5; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.5e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVHSLARACKV 12
 DB 73 KVHSLARACKV 84

RESULT 12
 09S9J0 PRELIMINARY; PRT; 309 AA.
 AC 09S9J0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE T23K8.1 (Fragment).
 GN T23K8.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA Vysotskaya V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
 RA Li J., Kremenetskaia I., Ngan I., Luros J., Gonzalez A., Altafi H.,
 RA Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
 RA Huizar L., Kim C., Palm C.J., Rowley D., Shinn P., Walker M.,
 RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
 RT "Arabidopsis thaliana chromosome 1 BAC T23K8 sequence.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA Theologis A.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC007230; AAD26867.1; -.
 FT NON_TER 309
 SQ SEQUENCE 309 AA; 34049 MW; 4FF1D7AF877A0D1 CRC64;
 Query Match 15.3%; Score 9; DB 10; Length 309;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 KKKKKTGRA 32
 DB 232 KKKKKTGRA 240

RESULT 13
 0971R7 PRELIMINARY; PRT; 135 AA.
 AC 0971R7;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE Uncharacterized protein, yJDF B. subtilis ortholog.
 GN CAC1573.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiales; Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Neelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Olu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe P., Doucet-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AE007667; AAK79540.1; -.
 KW Complete proteome.
 SQ SEQUENCE 135 AA; 16388 MW; 387D5F8D11444E7A CRC64;
 Query Match 13.6%; Score 8; DB 16; Length 135;
 Best Local Similarity 100.0%; Pred. No. 0.79;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 21 KKKKKKK 28
 DB 124 KKKKKKK 131

RESULT 14

Q9L657 PRELIMINARY; PRT; 134 AA.
 AC Q9L657;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE Histone-like nucleoid structuring protein.
 GN HNS.
 OS Proteus mirabilis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Proteus.
 OX NCBI_TaxID=584;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H1320;
 RA Coker C., Bakare O.O., Mobley H.L.T.;
 RT "H-NS is a Repressor of the Proteus mirabilis Urease Transcriptional
 RT Activator Gene ureR";
 RL J. Bacteriol. 0:0-0(2000).
 DR EMBL: AF240693; AAF61240.1; -.
 DR HSSP: P08936; 1HNR.
 DR InterPro: IPR001801; Histone_HNS.
 DR Pfam: PF00816; Histone_HNS.1
 DR PRODOM: PD007337; Histone_HNS.1
 DR SMART: SM00528; HNS.1
 SQ SEQUENCE 134 AA; 15249 MW; 202C49BCA12597B3 CRC64;

Query Match 11.9%; Score 7; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 KTGRAKR 34
 |||||
 Db 83 KTGRAKR 89

RESULT 15

O9RSE5 PRELIMINARY; PRT; 154 AA.
 ID O9RSE5
 AC O9RSE5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE Hypothetical protein DR2179.
 GN DR2179.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 CC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RL;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Uitterlinden T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith R.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome Sequence of the radioresistant bacterium Deinococcus
 RT radiodurans RL";
 RL Science 286:1571-1577(1999).
 DR EMBL: AE002051; AAF11732.1; -.
 DR TIGR: DR2179; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 154 AA; 16181 MW; 58AA86884AA0D4C4 CRC64;

Query Match 11.9%; Score 7; DB 16; Length 154;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RAGKVG 14
 |||||
 Db 39 RAGKVG 45

RESULT 16

O9NBB4 PRELIMINARY; PRT; 157 AA.
 ID O9NBB4
 AC O9NBB4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE Stretchin-MICK (Fragment)
 GN STRN-MICK OR CG8304 OR CG18255.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Champagne M.B., Edwards K.A., Erickson H.P., Kiehart D.P.;
 RT "Drosophila stretchin-MICK is a Novel Member of the Titin/Myosin Light
 RT Chain Kinase Family";
 RL J. Mol. Biol. 0:0-0(2000).
 DR EMBL: AF257306; AAF90124.1; -.
 DR FlyBase: FBgn0013988; Strn-MICK.
 FT NON_TER 1 157
 FT NON_TER 1 157
 SQ SEQUENCE 157 AA; 18077 MW; 0C73A2D3AE35278F CRC64;

Query Match 11.9%; Score 7; DB 5; Length 157;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKKT 29
 |||||
 Db 150 EKKKKKT 156

RESULT 17

O9ZOB1 PRELIMINARY; PRT; 173 AA.
 ID O9ZOB1
 AC O9ZOB1;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE Putative DNA binding protein with homeobox domain.
 GN ATG36610.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA.
 RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
 RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
 RA Carreira A.J., Cressy T.H., Buell C.R., Town C.D., Nierman W.C.,
 RA Fraser C.M., Venter J.C.;
 RT Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC006282; AAD20137.2; -.
 DR EMBL: AC006919; AAM15313.1; -.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 173 AA; 20478 MW; 57A67DCDA47E75FF CRC64;

Query Match 11.9%; Score 7; DB 10; Length 173;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 OEKKKKK 28
 |||||

Db 42 OEKKKKG 48

RESULT 18

Q9AGU8 PRELIMINARY; PRT; 198 AA.
AC Q9AGU8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Biotin carboxyl carrier protein (Fragment).
GN ACCB.
OS Brucella abortus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2308;
RA Essenberg R.C.;
RT "Cloning and sequence of the arcd gene of Brucella abortus.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF326476; AAK27449.1; -
DR HSSP: P02905; 3BDO.
DR InterPro: IPR001249; ACGBA_biotinCC.
DR InterPro: IPR001882; Biotin_attach.
DR InterPro: IPR000089; Biotin_11poyl.
DR Pfam: PF00364; Biotin_11poyl.1.
DR PRINTS: PR01071; ACGBA_biotinCC.
DR TIGRfams: TIGR00531; BCCP.1.
DR PROSITE: PS00188; BIOTIN; UNKNOWN_1.
FT NON_TER 198
SQ SEQUENCE 198 AA; 20832 MW; D6CB392B2D4146F2 CRC64;

Query Match 11.9%; Score 7; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
IIIIIIII
Db 40 KKKKKTG 46

RESULT 19

Q64075 PRELIMINARY; PRT; 215 AA.
AC Q64075;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Nucleoporin p62 homolog protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95151924; Pubmed=7849178;
RA Wang Z.Q., Akmal K.M., Kim K.H.;
RT "An unusual nucleoporin-related messenger ribonucleic acid is present
in the germ cells of rat testis.";
RL Biol. Reprod. 51:1022-1030(1994).
DR EMBL: S75997; AAB33384.1; -
KW Porin.
FT NON_TER 1
SQ SEQUENCE 215 AA; 24593 MW; 098251C97A8FBD88 CRC64;

Query Match 11.9%; Score 7; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
IIIIIIII

Db 52 KKKKKTG 58

RESULT 20

Q9LIR5 PRELIMINARY; PRT; 224 AA.
AC Q9LIR5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Genomic DNA, chromosome 3, BAC clone:FL4013.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsids.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneke T., Kato T., Sato S., Nakamura Y., Asanizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; Pubmed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety P1,
TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL: AP001297; BAB03010.1; -
SQ SEQUENCE 224 AA; 26999 MW; D4DFC32657C0A125 CRC64;

Query Match 11.9%; Score 7; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
IIIIIIII
Db 200 KKKKKTG 206

RESULT 21

Q9FZ76 PRELIMINARY; PRT; 233 AA.
AC Q9FZ76;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative 60S ribosomal protein L6 (Putative 60S ribosomal protein
L6).
GN F2516.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC Federapfel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA Buehler E., Chao Q., Chin C., Chou J., Choi E., Gonzalez A.,
RA Hwang B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA Lenz C., Liu A., Liu S., Mukharly N., Pham P., Sakano H., Shinn P.,
RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Bann J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

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RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC062328; AAF98420.1; -
DR EMBL; AY054675; AAK96866.1; -
DR EMBL; AY072496; AAL66911.1; -
DR InterPro; IPR000915; Ribosomal_L6E.
DR Pfam; PF01159; Ribosomal_L6E; 1.
DR ProDom; PD009612; Ribosomal_L6E; 1.
KW Ribosomal protein.
SQ SEQUENCE 233 AA; 26153 MW; 1ED96B26A0F85CB CRC64;

Query Match 11.9%; Score 7; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKKT 29
Db 166 EKKKKKT 172

RESULT 22
Q9C9C6 PRELIMINARY; PRT; 233 AA.
ID Q9C9C6;
AC Q9C9C6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative 60S ribosomal protein L6.
GN F2P9.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-CV. COLUMBIA;
RX MEDLINE-21016719; PubMed-11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dwar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Mafti R., Marshall A.,
RA Miltischer J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotska V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RA thaliana."
RL Nature 408:816-820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
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RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC016662; AAG52524.1; -
DR EMBL; AY062622; AAL32700.1; -
DR InterPro; IPR000915; Ribosomal_L6E.
DR Pfam; PF01159; Ribosomal_L6E; 1.
DR ProDom; PD009612; Ribosomal_L6E; 1.
KW Ribosomal protein.
SQ SEQUENCE 233 AA; 26008 MW; 837890EFA8082A40 CRC64;

Query Match 11.9%; Score 7; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKKT 29
Db 166 EKKKKKT 172

RESULT 23
Q9C9C5 PRELIMINARY; PRT; 233 AA.
ID Q9C9C5;
AC Q9C9C5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative 60S ribosomal protein L6.
GN F2P9.8 OR ATIG74050.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-CV. COLUMBIA;
RX MEDLINE-21016719; PubMed-11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dwar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Mafti R., Marshall A.,
RA Miltischer J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotska V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RA thaliana."
RL Nature 408:816-820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
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RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC016662; AAG52527.1; -
 DR EMBL: AY054573; AAG96764.1; -
 DR EMBL: AY081305; AAL91194.1; -
 DR InterPro: IPR000915; Ribosomal_L6E.
 DR Pfam: PF01159; Ribosomal_L6E; 1.
 DR ProDom: PD009612; Ribosomal_L6E; 1.
 KW Ribosomal protein.

SO SEQUENCE 233 AA; 26107 MW; 77268505F51280EA CRC64;

Query Match 11.9%; Score 7; DB 10; Length 233;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKKT 29
 DB 166 EKKKKKT 172

RESULT 24

Q9AD23 PRELIMINARY; PRT; 259 AA.

AC Q9AD23;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein SCPI.127.
 CN SCPI.127.
 OS Streptomyces coelicolor.
 OG Plasmid SCPI.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL590463; CAC36648.1; -
 KW Hypothetical protein: Plasmid.
 SO SEQUENCE 259 AA; 28708 MW; 357BF1A6821CFE5F CRC64;

Query Match 11.9%; Score 7; DB 16; Length 259;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 11
 DB 127 SLARAG 133

RESULT 25

Q9NSK3 PRELIMINARY; PRT; 283 AA.

AC Q9NSK3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE Hypothetical 31.4 kDa protein (Fragment).
 GN DKFZP621166.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MELANOMA;
 RA Bloecker H., Boecker M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL162072; CAB82408.1; -
 KW Hypothetical protein.
 FT NON_TER 1

SO SEQUENCE 283 AA; 31436 MW; 3E3782A2086E9EB CRC64;

Query Match 11.9%; Score 7; DB 4; Length 283;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSLARAG 10
 DB 236 GSLARAG 242

RESULT 26

Q95T41 PRELIMINARY; PRT; 309 AA.

AC Q95T41;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE GH23743P.
 GN CG3441.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY060340; AAL25379.1; -
 DR FlyBase: FBgn0035092; CG3441.
 SO SEQUENCE 309 AA; 34197 MW; 620BB8A464BEF487 CRC64;

Query Match 11.9%; Score 7; DB 5; Length 309;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSLARAG 10
 DB 153 GSLARAG 159

RESULT 27

O66535 PRELIMINARY; PRT; 314 AA.

AC O66535;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Riboflavin kinase.
 GN RIBF OR AO_139.
 OS Aquifex aeolicus.
 CC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 CN NCBI_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,

RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus";
 RL Nature 392:353-358(1998).
 DR EMBL: AE000675; AAC06488.1; -;
 DR InterPro: IPR002606; FAD_Synth.
 DR Pfam: PF01687; FAD_Synth. 1.
 DR ProDom: PD003662; FAD_Synth. 1.
 DR TIGRFAMs: TIGR00083; rldf. 1.
 KW Complete proteome.
 SQ SEQUENCE 314 AA; 36660 MW; 81F8B09671CE70E5 CRC64;

Query Match 11.9%; Score 7; DB 16; Length 314;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 PTFGKKK 53
 DB 253 PTFGKKK 259

RESULT 28

Q95XC7 PRELIMINARY; PRT; 339 AA.
 ID Q95XC7;
 AC Q95XC7;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Hypothetical 37.3 kDa protein.
 GN Y73B6BL.31.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Graves T.;
 RT "The sequence of C. elegans cosmid Y73B6BL.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC084197; AAL00874.2; -;
 DR InterPro: IPR000620; DUF6.
 DR Pfam: PF00892; DUF6. 1.
 KW Hypothetical protein.
 SQ SEQUENCE 339 AA; 37344 MW; 6793E7D389006C31 CRC64;

Query Match 11.9%; Score 7; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TFGKKK 54
 DB 91 TFGKKK 97

RESULT 29

Q96GN4 PRELIMINARY; PRT; 380 AA.
 ID Q96GN4

AC Q96GN4;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Similar to kinesin family member 5B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-CELL;
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC009353; AAH09353.1; -;
 DR InterPro: IPR001752; kinesin_motor.
 DR Pfam: PF00225; kinesin. 1.
 DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1.
 DR PROSITE: PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Coiled coil; Microtubules; Motor protein.
 SQ SEQUENCE 380 AA; 43059 MW; 912B4E7371C23650 CRC64;

Query Match 11.9%; Score 7; DB 4; Length 380;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKKT 29
 DB 345 EKKKKKT 351

RESULT 30

Q9W0W6 PRELIMINARY; PRT; 380 AA.
 ID Q9W0W6;
 AC Q9W0W6;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE CG3441 protein.
 GN CG3441.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sulten G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Abmayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster A., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegun C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketcho K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Stimpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003466; AAF47313.1; -;
 DR Flybase: FBgn0035092; CG3441.
 SQ SEQUENCE 380 AA; 41734 MW; 35722F8707289C3F CRC64;

Query Match 11.9%; Score 7; DB 5; Length 380;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSILRAG 10
 |||||
 DB 153 GSILRAG 159

RESULT 31
 Q15694 PRELIMINARY; PRT; 381 AA.
 ID Q15694
 AC Q15694;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE Protein immuno-reactive with anti-PTH polyclonal antibodies
 OS (Fragment).
 DE Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96187433; Pubmed=8608414;
 RA Kumar R., Haugen J.D., Wieben E.D., Londowski J.M., Cai Q.;
 RT "Inhibitors of renal epithelial phosphate transport in tumor-induced
 RL osteomalacia and uremia.";
 RT Proc. Assoc. Am. Physicians 107:296-305(1995).
 DR EMBL: U28831; AAB02177.1; -;
 FT NON_TER 1
 FT NON_TER 381
 SQ SEQUENCE 381 AA; 42574 MW; BFE144AB3A21C6DD CRC64;

Query Match 11.9%; Score 7; DB 4; Length 381;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 OEKKKK 28
 |||||
 DB 375 OEKKKK 381

RESULT 32
 Q9S2F0 PRELIMINARY; PRT; 424 AA.
 ID Q9S2F0
 AC Q9S2F0;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Putative ABC transporter ATP-binding protein.
 GN SCO2931 OR SCB19A.31.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Seeger K., Harris D.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE=97000351; Pubmed=8843436;
 RA Redendach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RL the 8 Mb streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RL coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL: AL096852; CAB51012.1; -;
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR000644; CBS_domain.
 DR Pfam: PF00005; ABC_tran; 1.
 DR Pfam: PF00571; CBS; 2.
 DR ProDom: PD000006; ABC_transporter; 1.
 DR SMART: SM00382; AAA; 1.
 DR TIGRfams: TIGR01186; prov; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport.
 KW SEQUENCE 424 AA; 46529 MW; BE6B1D3D89BFF1E CRC64;

Query Match 11.9%; Score 7; DB 16; Length 424;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSILRAG 10
 |||||
 DB 328 GSILRAG 334

RESULT 33
 Q9X4J1 PRELIMINARY; PRT; 429 AA.
 ID Q9X4J1
 AC Q9X4J1;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Provl.
 GN PROVL.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-M145;
 RA Tan H., Tian Y., Yang H., Chater K.F.;
 RT "Study on a proU-like operon which related to glycine-betaine
 transport of *Streptomyces coelicolor*";
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
 CC -1. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL: AF112365; AAD29279.1; -.
 DR InterPro: IPR003593; AAA_Arpase.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR000644; CBS_domain.
 DR Pfam: PF000571; ABC_tran; 1.
 DR ProDom: PD000006; ABC_transport; 1.
 DR SMART: SM00382; AAA; 1.
 DR TIGRFAMs: TIGR01186; proV; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 DR ATP-binding; Transport.
 SQ SEQUENCE 429 AA; 47360 MW; 9053C61CAB5A4484 CRC64;

Query Match 11.9%; Score 7; DB 2; Length 429;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSIARAG 10
 DB 333 GSIARAG 339

RESULT 34
 O9K509 PRELIMINARY; PRT; 454 AA.
 AC O9K509;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Replicative DNA helicase.
 GN DMC OR BH4029.
 OS *Bacillus halodurans*.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_Taxid=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 /JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
 RT *halodurans* and genomic sequence comparison with *Bacillus subtilis*."
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL: AP001520; BAB07748.1; -.
 DR HSSP: P03005; LME.
 DR InterPro: IPR001198; Dnab_helicase.
 DR Pfam: PF00772; Dnab; 1.
 DR TIGRFAMs: TIGR00065; Dnab; 1.
 DR Helicase; Complete proteome.
 SQ SEQUENCE 454 AA; 50630 MW; D9D6DE17A52EAD3A CRC64;

Query Match 11.9%; Score 7; DB 16; Length 454;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSIARAG 10
 DB 281 GSIARAG 287

RESULT 35
 O91290 PRELIMINARY; PRT; 542 AA.
 AC O91290;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Heat shock protein 90 (Fragment).
 GN HSC90.
 OS *Pleurodeles waltl* (Iberian ribbed newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
 OC Pleurodeles.
 OX NCBI_Taxid=8319;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95246904; PubMed=7729567;
 RA Coumilleau P., Billoud B., Sourrouille P., Moreau N., Angelier N.;
 RT "Evidence for a 90 kDa heat-shock protein gene expression in the
 RT amphibian oocyte."
 RL Dev. Biol. 166:247-258(1995).
 DR EMBL: U32987; AAA92343.1; -.
 DR HSSP: P07900; 1YER.
 DR InterPro: IPR001404; Hsp90.
 DR Pfam: PF00183; HSP90; 1.
 FT NON_TER 1
 SQ SEQUENCE 542 AA; 63096 MW; E2FAEAB9250C2626 CRC64;

Query Match 11.9%; Score 7; DB 13; Length 542;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKKT 29
 DB 81 EKKKKKT 87

RESULT 36
 O9NXU4 PRELIMINARY; PRT; 576 AA.
 AC O9NXU4;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE CDNA FLJ20052 fis, clone COL00777 (Fragment).
 OS *Homo sapiens* (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Kawabata A., Hiki J. T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isonaga T., Sugano S.;
 RT "NEO human cDNA sequencing project."
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AK000059; BAA90916.1; -.
 DR HSSP: P17119; 3KAR.
 DR InterPro: IPR001752; kinesin_motor.
 DR Pfam: PF00225; kinesin; 1.
 DR PRINTS: PR00380; KINESINHEAVY.
 DR SMART: SM00129; KISC; 1.
 DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
 DR KINASE: P550067; KINESIN_MOTOR_DOMAIN2; 1.
 DR ATP-binding; Coiled coil; Microtubules; Motor protein.
 FT NON_TER 576
 SQ SEQUENCE 576 AA; 64518 MW; A21BBE950F4946D6 CRC64;

Query Match 11.9%; Score 7; DB 4; Length 576;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 OEKKKKK 28
 DB 570 OEKKKKK 576

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RESULT 37
098CL9 PRELIMINARY; PRT; 594 AA.
AC 098CL9;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Two-component sensor histidine kinase, Exos.
GN MLL5094.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabeta S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
    Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL: AP003005; BAB51602.1;
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR003660; HAMp.
DR InterPro: IPR003661; His_kinA.
DR InterPro: IPR004359; His_Kin_slg.
DR Pfam: PF00672; HAMp. 1.
DR Pfam: PF02518; HAMpase_C. 1.
DR Pfam: PF00512; signal. 1.
DR PRINTS: PR00344; BCTRSENSOR.
DR SMART: SM00304; HAMp. 1.
DR SMART: SM00387; HAMpase_C. 1.
DR SMART: SM00386; HisK. 1.
KW kinase; Complete proteome.
SQ SEQUENCE 594 AA; 65169 MW; EDE20CFA78D72819 CRC64;

Query Match 11.9%; Score 7; DB 16; Length 594;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARACK 11
    |||||
Db 505 SLARACK 511

RESULT 38
09M8T5 PRELIMINARY; PRT; 806 AA.
AC 09M8T5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F13E7.12 protein.
GN F13E7.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Ronald C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F13E7 genomic sequence.";
    Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC018163; AAF26966.1;

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DR InterPro: IPR000875; Cecropin.
DR InterPro: IPR000533; Tropomyosin.
DR PRINTS: PR00194; TROPOMYOSIN.
DR PROSITE: PS00268; CECROPIN; UNKNOWN_1.
SQ SEQUENCE 806 AA; 91859 MW; AFE6F9AED5D4BFD CRC64;

Query Match 11.9%; Score 7; DB 10; Length 806;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKKT 29
    |||||
Db 782 EKKKKKT 788

RESULT 39
09M0D8 PRELIMINARY; PRT; 863 AA.
AC 09M0D8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Serine/threonine-specific receptor protein kinase-11k protein.
GN A74G29450.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
    Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AL161575; CAB79703.1;
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002896; Herpes_glycop_D.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; TYR_pkinase.
DR Pfam: PF01537; Herpes_glycop_D. 1.
DR Pfam: PF00560; LRR. 2.
DR Pfam: PF00069; pkinase. 1.
DR PRINTS: PR01651; SECCEXPOR.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Euk_pkinase. 1.
DR SMART: SM00370; LRR. 2.
DR SMART: SM00221; STYKc. 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST. 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
    transferase.
SQ SEQUENCE 863 AA; 96557 MW; 32AE253F9C708427 CRC64;

Query Match 11.9%; Score 7; DB 10; Length 863;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QEKKKKK 28
    |||||
Db 504 QEKKKKK 510

RESULT 40
09MC26

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ID 09WC26 PRELIMINARY; PRT; 1254 AA.
AC 09WC26;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Structural polyprotein.
OS Venezuelan equine encephalitis virus (strain Mena II).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=36384;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MENA II;
RA MEDLINE-99101297; PubMed-9886206;
RA Kinney R.M., Pfeffer M., Tsuchiya K.R., Chang G.J., Roehrig J.T.;
RT "Nucleotide sequences of the 26S mRNAs of the viruses defining the
RT Venezuelan equine encephalitis antigenic complex.";
RL Am. J. Trop. Med. Hyg. 59:952-964(1998).
RM [2]
RN SEQUENCE FROM N.A.
RC STRAIN-MENA II;
RA Kinney R.M., Pfeffer M., Weissner J.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075252; AAD14553.1; -.
DR HSP; P03315; IYCP.
DR InterPro; IPR001836; Alpha_core.
DR InterPro; IPR002548; Alpha_E1_glycop.
DR InterPro; IPR000936; Alpha_E2_glycop.
DR InterPro; IPR002533; Alpha_E3_glycop.
DR InterPro; IPR000930; Togavirin.
DR Pfam; PF00944; Alpha_core; 1.
DR Pfam; PF01589; Alpha_E1_glycop; 1.
DR Pfam; PF00943; Alpha_E2_glycop; 1.
DR Pfam; PF01563; Alpha_E3_glycop; 1.
DR PRINTS; PR00798; TOGAVIRIN.
KW Polyprotein.
FT CHAIN 1 274 NUCLEOCAPSID PROTEIN.
FT CHAIN 275 333 POLYPROTEIN CLEAVAGE PRODUCT E3.
FT CHAIN 334 756 ENVELOPE GLYCOPROTEIN 2.
FT CHAIN 757 812 6K POLYPROTEIN CLEAVAGE PRODUCT.
FT CHAIN 813 1254 ENVELOPE GLYCOPROTEIN 1.
SQ SEQUENCE 1254 AA; 138329 MW; 0E3321D41F4DE39 CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1254;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 KKKKRTG 30
Db 88 KKKKRTG 94

RESULT 41
O9YKD3 PRELIMINARY; PRT; 1254 AA.
AC O9YKD3;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Structural polyprotein.
OS Venezuelan equine encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11036;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-96347778; PubMed-9684636;
RA Oberste M.S., Fraile M., Navarro R., Zepeda C., Zarate M.L.,
RA Ludwig G.V., Kondig J.F., Weaver S.C., Smith J.F., Rico-Hesse R.;
RT "Association of Venezuelan equine encephalitis virus subtype IE with
RT two equine epizootics in Mexico.";
RL Am. J. Trop. Med. Hyg. 59:100-107(1998).
RM [2]
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RP SEQUENCE FROM N.A.
RC STRAIN-OAX142;
RX MEDLINE-21657447; PubMed-11799167;
RA Brault A.C., Powers A.M., Holmes E.C., Woelk C.H., Weaver S.C.;
RT "Positively charged amino acid substitutions in the E2 envelope
RT glycoprotein are associated with the emergence of Venezuelan equine
RT encephalitis virus.";
RL J. Virol. 76:1718-1730(2002).
DR EMBL; U96408; AAD19216.1; -.
DR EMBL; AF448538; AAL47153.1; -.
DR HSP; P03315; IYCP.
DR MEROPS; S03.001; -.
DR InterPro; IPR001836; Alpha_core.
DR InterPro; IPR002548; Alpha_E1_glycop.
DR InterPro; IPR000936; Alpha_E2_glycop.
DR InterPro; IPR002533; Alpha_E3_glycop.
DR InterPro; IPR000930; Togavirin.
DR Pfam; PF00944; Alpha_core; 1.
DR Pfam; PF01589; Alpha_E1_glycop; 1.
DR Pfam; PF00943; Alpha_E2_glycop; 1.
DR Pfam; PF01563; Alpha_E3_glycop; 1.
DR PRINTS; PR00798; TOGAVIRIN.
KW Polyprotein.
SQ SEQUENCE 1254 AA; 138377 MW; C07D6844531DA587 CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1254;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 KKKKRTG 30
Db 88 KKKKRTG 94

RESULT 42
O88979 PRELIMINARY; PRT; 1254 AA.
AC O88979;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Structural polyprotein.
OS Venezuelan equine encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-680201;
RX MEDLINE-96204604; PubMed-8623548;
RA Oberste M.S., Parker M.D., Smith J.F.;
RT "Complete sequence of Venezuelan equine encephalitis virus subtype IE
RT reveals conserved and hypervariable domains within the C terminus of
RT nsP3.";
RL Virology 219:314-320(1996).
DR EMBL; U34999; AAB04683.1; -.
DR HSP; P03315; IYCP.
DR InterPro; IPR001836; Alpha_core.
DR InterPro; IPR002548; Alpha_E1_glycop.
DR InterPro; IPR000936; Alpha_E2_glycop.
DR InterPro; IPR002533; Alpha_E3_glycop.
DR InterPro; IPR000930; Togavirin.
DR Pfam; PF00944; Alpha_core; 1.
DR Pfam; PF01589; Alpha_E1_glycop; 1.
DR Pfam; PF00943; Alpha_E2_glycop; 1.
DR Pfam; PF01563; Alpha_E3_glycop; 1.
DR PRINTS; PR00798; TOGAVIRIN.
KW Polyprotein.
SQ SEQUENCE 1254 AA; 138258 MW; BFFB9F3BD6C99C1 CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1254;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 24 KKKKKTG 30
 |||||
 DB 88 KKKKKTG 94

RESULT 43

Q8V293
 ID 08V293 PRELIMINARY; PRT: 1254 AA.

AC 08V293;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Structural polyprotein.
 OS Venezuelan equine encephalitis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 NC NCBL_TaxID=11036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CPA201;
 RX MEDLINE=21657447; PubMed=11799167;
 RA Brault A.C., Powers A.M., Holmes E.C., Woelk C.H., Weaver S.C.;
 RT "Positively charged amino acid substitutions in the E2 envelope glycoprotein are associated with the emergence of Venezuelan equine encephalitis virus."
 RT J. Virol. 76:1718-1730(2002).
 RL EMBL: AF448537; AAL47151.1; -.
 DR EMBL: AF448537; AAL47151.1; -.
 DR InterPro: IPR001836; Alpha_E1-glycop.
 DR InterPro: IPR002548; Alpha_E1-glycop.
 DR InterPro: IPR000936; Alpha_E2-glycop.
 DR InterPro: IPR002533; Alpha_E3-glycop.
 DR InterPro: IPR000930; Togavirin.
 DR Pfam: PF00944; Alpha_Core; 1.
 DR Pfam: PF01589; Alpha_E1-glycop; 1.
 DR Pfam: PF00943; Alpha_E2-glycop; 1.
 DR Pfam: PF01563; Alpha_E3-glycop; 1.
 DR PRINTS: PR00798; TOGAVIRIN.
 KW Polyprotein.
 SQ SEQUENCE 1254 AA: 138376 MW; E024103E7F6B0FD4 CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
 |||||
 DB 88 KKKKKTG 94

RESULT 44

Q8V291
 ID 08V291 PRELIMINARY; PRT: 1254 AA.

AC 08V291;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Structural polyprotein.
 OS Venezuelan equine encephalitis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 NC NCBL_TaxID=11036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=80U76;
 RX MEDLINE=21657447; PubMed=11799167;
 RA Brault A.C., Powers A.M., Holmes E.C., Woelk C.H., Weaver S.C.;
 RT "Positively charged amino acid substitutions in the E2 envelope glycoprotein are associated with the emergence of Venezuelan equine encephalitis virus."
 RT J. Virol. 76:1718-1730(2002).
 RL EMBL: AF448539; AAL47155.1; -.
 DR EMBL: AF448539; AAL47155.1; -.
 DR InterPro: IPR001836; Alpha_Core.

DR InterPro: IPR002548; Alpha_E1-glycop.
 DR InterPro: IPR000936; Alpha_E2-glycop.
 DR InterPro: IPR002533; Alpha_E3-glycop.
 DR InterPro: IPR000930; Togavirin.
 DR Pfam: PF00944; Alpha_Core; 1.
 DR Pfam: PF01589; Alpha_E1-glycop; 1.
 DR Pfam: PF00943; Alpha_E2-glycop; 1.
 DR Pfam: PF01563; Alpha_E3-glycop; 1.
 DR PRINTS: PR00798; TOGAVIRIN.
 KW Polyprotein.
 SQ SEQUENCE 1254 AA: 138341 MW; 6EC946B80BEA6817 CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
 |||||
 DB 88 KKKKKTG 94

RESULT 45

Q8UYH1
 ID 08UYH1 PRELIMINARY; PRT: 1264 AA.

AC 08UYH1;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Structural polyprotein.
 OS Venezuelan equine encephalitis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 NC NCBL_TaxID=11036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OAX131, AND CPA152;
 RX MEDLINE=21657447; PubMed=11799167;
 RA Brault A.C., Powers A.M., Holmes E.C., Woelk C.H., Weaver S.C.;
 RT "Positively charged amino acid substitutions in the E2 envelope glycoprotein are associated with the emergence of Venezuelan equine encephalitis virus."
 RT J. Virol. 76:1718-1730(2002).
 RL EMBL: AF448535; AAL47149.1; -.
 DR EMBL: AF448535; AAL47149.1; -.
 DR InterPro: IPR001836; Alpha_Core.
 DR InterPro: IPR002548; Alpha_E1-glycop.
 DR InterPro: IPR000936; Alpha_E2-glycop.
 DR InterPro: IPR002533; Alpha_E3-glycop.
 DR InterPro: IPR000930; Togavirin.
 DR Pfam: PF00944; Alpha_Core; 1.
 DR Pfam: PF01589; Alpha_E1-glycop; 1.
 DR Pfam: PF00943; Alpha_E2-glycop; 1.
 DR Pfam: PF01563; Alpha_E3-glycop; 1.
 DR PRINTS: PR00798; TOGAVIRIN.
 KW Polyprotein.
 SQ SEQUENCE 1264 AA: 139454 MW; 39DBF8657BDADF7F CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1264;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
 |||||
 DB 98 KKKKKTG 104

Search completed: February 6, 2003, 21:31:48
 Job time : 33 secs

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OM protein - protein search, using sw model

Run on: February 6, 2003, 21:30:59 : Search time 15 seconds
(without alignments)
115.730 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59
Sequence: 1 KKHSLARAGKVRGQTPKVA.....RRFVVVPTFFGKKKGPNNMS 59

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7	11.9	381	1	US-08-487-810-2	Sequence 2, Appl1
2	7	11.9	409	2	US-08-743-130A-2	Sequence 2, Appl1
3	7	11.9	409	2	US-08-743-130A-39	Sequence 39, Appl1
4	7	11.9	7257	3	US-09-335-409-5	Sequence 5, Appl1
5	7	11.9	7257	4	US-09-568-102-5	Sequence 5, Appl1
6	7	11.9	7257	4	US-09-567-969-5	Sequence 5, Appl1
7	7	11.9	7257	4	US-09-568-480-5	Sequence 5, Appl1
8	7	11.9	7257	4	US-09-568-486-5	Sequence 5, Appl1
9	7	11.9	7257	4	US-09-568-472-5	Sequence 5, Appl1
10	7	11.9	7257	4	US-09-567-899-5	Sequence 5, Appl1
11	6	10.2	15	4	US-09-082-358B-24	Sequence 24, Appl1
12	6	10.2	15	4	US-09-082-358B-62	Sequence 62, Appl1
13	6	10.2	16	3	US-08-851-843A-201	Sequence 201, App
14	6	10.2	16	4	US-08-974-549A-320	Sequence 320, App
15	6	10.2	16	4	US-08-854-050-201	Sequence 201, App
16	6	10.2	16	4	US-09-430-323-201	Sequence 201, App
17	6	10.2	29	4	US-09-177-249-189	Sequence 189, App
18	6	10.2	51	4	US-09-227-357-479	Sequence 479, App
19	6	10.2	55	4	US-08-569-749-5	Sequence 5, Appl1
20	6	10.2	55	4	US-08-569-749-6	Sequence 6, Appl1
21	6	10.2	55	5	PCT-US96-12860-5	Sequence 5, Appl1
22	6	10.2	57	4	PCT-US96-12860-6	Sequence 6, Appl1
23	6	10.2	57	4	US-09-082-358B-43	Sequence 43, Appl1
24	6	10.2	63	4	US-08-971-089-2	Sequence 2, Appl1
25	6	10.2	68	2	US-08-511-485-18	Sequence 18, Appl1
26	6	10.2	68	2	US-08-511-485-19	Sequence 19, Appl1
27	6	10.2	141	4	US-09-091-725-51	Sequence 51, Appl1

28	6	10.2	154	4	US-08-871-732A-1	Sequence 1, Appl1
29	6	10.2	154	4	US-09-346-510B-1	Sequence 1, Appl1
30	6	10.2	175	2	US-08-533-669A-4	Sequence 4, Appl1
31	6	10.2	175	4	US-09-183-861-4	Sequence 4, Appl1
32	6	10.2	175	4	US-09-022-765-4	Sequence 4, Appl1
33	6	10.2	197	1	US-08-468-347-24	Sequence 24, Appl1
34	6	10.2	197	2	US-08-467-389-24	Sequence 24, Appl1
35	6	10.2	197	2	US-08-779-379-24	Sequence 24, Appl1
36	6	10.2	197	2	US-08-469-219-24	Sequence 24, Appl1
37	6	10.2	197	4	US-09-228-152-24	Sequence 24, Appl1
38	6	10.2	234	2	US-08-903-801-3	Sequence 3, Appl1
39	6	10.2	234	4	US-09-295-055-3	Sequence 3, Appl1
40	6	10.2	251	4	US-09-149-476-568	Sequence 568, App
41	6	10.2	316	4	US-09-347-803-20	Sequence 20, Appl1
42	6	10.2	318	4	US-09-615-192A-389	Sequence 389, App
43	6	10.2	341	4	US-09-347-803-16	Sequence 16, Appl1
44	6	10.2	370	2	US-08-729-214-27	Sequence 27, Appl1
45	6	10.2	370	3	US-09-028-934-27	Sequence 27, Appl1

ALIGNMENTS

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RESULT 1
US-08-487-810-2
; Sequence 2, Application US/08487810
; Patent No. 5618695
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA ENCODING HEM-1, A GENE EXPRESSED BY
; TITLE OF INVENTION: SCLEROSING HEMANGIOMA CELLS
; NUMBER OF SEQUENCES: 2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-810-2

Query Match      11.9%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      22 OEKKKK 28
Db      375 OEKKKK 381

RESULT 2
US-08-743-130A-2
; Sequence 2, Application US/08743130A
; Patent No. 5871987
; GENERAL INFORMATION:
; APPLICANT: Sassanfar, Mandana
; APPLICANT: Gallant, Paul L.
; APPLICANT: Shen, Xiaoyu
; APPLICANT: Tao, Nianjun
; APPLICANT: Tao, Jianshi
; APPLICANT: Houman, Fariba
; TITLE OF INVENTION: CANDIDA TYROSYL-TRNA SYNTHETASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
```

```
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CPI95-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 409 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-743-130A-2

Query Match      11.9%; Score 7; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 KOEKKK 27
        |||||
DB      360 KOEKKK 366

RESULT 3
US-08-743-130A-39
Sequence 39, Application US/08743130A
Patent No. 5871987
GENERAL INFORMATION:
APPLICANT: Sassanfar, Mandana
APPLICANT: Gallant, Paul L.
APPLICANT: Shen, Xiaoyu
APPLICANT: Tao, Nianjun
APPLICANT: Tao, Jianshi
APPLICANT: Houman, Fariba
TITLE OF INVENTION: CANDIDA TYROSYL-TRNA SYNTHETASE
NUMBER OF INVENTION: 41
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.
CITY: Two Millitia Drive
STATE: Lexington
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CPI95-12
REFERENCE/DOCKET NUMBER: CPI95-12
```

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 409 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-743-130A-39

Query Match      11.9%; Score 7; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 KOEKKK 27
        |||||
DB      360 KOEKKK 366

RESULT 4
US-09-335-409-5
Sequence 5, Application US/09335409
Patent No. 6121029
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-335-409-5

Query Match      11.9%; Score 7; DB 3; Length 7257;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 STARAK 11
        |||||
DB      7250 STARAK 7256

RESULT 5
US-09-568-102-5
Sequence 5, Application US/09568102
Patent No. 6346404
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
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TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-568-102-5

Query Match 11.9%; Score 7; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAK 11
|||||||
Db 7250 SLARAK 7256

RESULT 6
US-09-567-969-5
Sequence 5, Application US/09567969
Patent No. 6355457
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-567-969-5

Query Match 11.9%; Score 7; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAK 11
|||||||
Db 7250 SLARAK 7256

RESULT 7
US-09-568-480-5
Sequence 5, Application US/09568480
Patent No. 6355458
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,480
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-568-480-5

Query Match 11.9%; Score 7; DB 4; Length 7257;

Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAK 11
|||||||
Db 7250 SLARAK 7256

RESULT 8
US-09-568-486-5
Sequence 5, Application US/09568486
Patent No. 6355459
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,486
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-568-486-5

Query Match 11.9%; Score 7; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAK 11
|||||||
Db 7250 SLARAK 7256

RESULT 9
US-09-568-472-5
Sequence 5, Application US/09568472
Patent No. 6358719
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,472
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-568-472-5

Query Match 11.9%; Score 7; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAK 11
|||||||

Db 7250 SLARACK 7256

RESULT 10

US-09-567-899-5
; Sequence 5, Application US/09567899; Patent No. 6383787
; GENERAL INFORMATION:

; APPLICANT: Schnupp, Thomas

; APPLICANT: Ligon, James

; APPLICANT: Molnar, Istvan

; APPLICANT: Zirkle, Ross

; APPLICANT: Cyr, Devon

; APPLICANT: Goerlach, Joern

; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

; FILE REFERENCE: 4-30582A

; CURRENT APPLICATION NUMBER: US/09/567,899

; CURRENT FILING DATE: 2000-05-10

; PRIOR FILING DATE: 1999-06-17

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 7257

; TYPE: PRT

; ORGANISM: Sorangium cellulosum

US-09-567-899-5

Query Match

Best local Similarity 100.0%; Score 7; DB 4; Length 7257;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARACK 11

Db 7250 SLARACK 7256

RESULT 11

US-09-082-358B-24
; Sequence 24, Application US/09082358B; Patent No. 6469153
; GENERAL INFORMATION:

; APPLICANT: Goff, Stephen P.

; APPLICANT: Li, Xingquiang

; TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,

; FILE REFERENCE: 0575/54804

; CURRENT APPLICATION NUMBER: US/09/082,358B

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 106

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24

; LENGTH: 15

; TYPE: PRT

; ORGANISM: murine

US-09-082-358B-24

Query Match

Best local Similarity 100.0%; Score 6; DB 4; Length 15;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28

Db 5 EKKKK 10

RESULT 12

US-09-082-358B-62
; Sequence 62, Application US/09082358B; Patent No. 6469153
; GENERAL INFORMATION:

; APPLICANT: Goff, Stephen P.

; APPLICANT: Li, Xingquiang

; TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,

; FILE REFERENCE: 0575/54804

; CURRENT APPLICATION NUMBER: US/09/082,358B

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 106

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 62

; LENGTH: 15

; TYPE: PRT

; ORGANISM: murine

US-09-082-358B-62

Query Match

Best local Similarity 100.0%; Score 6; DB 4; Length 15;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28

Db 10 EKKKK 15

RESULT 13

US-08-851-843A-201
; Sequence 201, Application US/08851843A; Patent No. 6093809
; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: No. 6093809e1 Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/851,843A

; FILING DATE: 06-MAY-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002930US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 201:

; SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-851-843A-201

Query Match 10.2%; Score 6; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||
Db 8 EKKKK 13

RESULT 14
US-08-974-549A-320
Sequence 320, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 320:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-320

Query Match 10.2%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||
Db 8 EKKKK 13

RESULT 15
US-08-854-050-201
Sequence 201, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00293005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-854-050-201

Query Match 10.2%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
|||||
Db 8 EKKKK 13

RESULT 16
US-09-430-323-201
Sequence 201, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morlin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00293005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 201:
US-09-430-323-201

Query Match 10.2%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
|||||
Db 8 EKKKK 13

RESULT 17
US-09-177-249-189
Sequence 189, Application US/09177249
Patent No. 6229064
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegarl, Ramlin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 189
LENGTH: 29
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-177-249-189

Query Match 10.2%; Score 6; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TFGKK 53
|||||
Db 1 TFGKK 6

RESULT 18
US-09-227-357-479
Sequence 479, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human secreted proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 479
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
US-09-227-357-479

Query Match 10.2%; Score 6; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 EKKKK 28

Db 35 EKKKK 40

RESULT 19
US-08-569-749-5
Sequence 5, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-5

Query Match 10.2%; Score 6; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLRAG 10
Db 22 SLRAG 27

RESULT 20
US-08-569-749-6
Sequence 6, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-6

Query Match 10.2%; Score 6; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAG 10
Db 22 SLARAG 27

RESULT 21

PCT-US96-12860-5
Sequence 5, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-5

Query Match 10.2%; Score 6; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAG 10
Db 22 SLARAG 27

RESULT 22

PCT-US96-12860-6
Sequence 6, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-6

Query Match 10.2%; Score 6; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAG 10
Db 22 SLARAG 27

RESULT 23

US-09-082-358B-43
Sequence 43, Application US/09082358B
Patent No. 6469153
GENERAL INFORMATION:
APPLICANT: Goff, Stephen P.
TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
FILE REFERENCE: 0575/54804
CURRENT APPLICATION NUMBER: US/09/082,358B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 106

SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 43
; LENGTH: 57
; TYPE: PRT
; ORGANISM: murine
US-09-082-358B-43

Query Match 10.2%: Score 6; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKK 29
Db 51 KKKKK 56

RESULT 24
US-08-971-089-2
; Sequence 2, Application US/08971089
; Patent No. 6376174
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Scoles, Daniel R.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING
; TITLE OF INVENTION: SCHWANNOMIN-BINDING-PROTEINS AND PRODUCTS RELATED THERETO
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,089
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,987
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramos, Robert T.
; REGISTRATION NUMBER: 37,915
; REFERENCE/DOCKET NUMBER: P-CE 2862
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-971-089-2

Query Match 10.2%: Score 6; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
Db 15 EKKKK 20

RESULT 25
US-08-511-485-18
; Sequence 18, Application US/08511485
; Patent No. 5919912

GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-18

Query Match 10.2%: Score 6; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 10
Db 21 SLARAG 26

RESULT 26
US-08-511-485-19
; Sequence 19, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-19

Query Match 10.2%; Score 6; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAG 10
Db 21 SLARAG 26

RESULT 27

US-09-091-725-51
Sequence 51, Application US/09091725
Patent No. 6329141

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Improved methods for transforming *Phaffia*
TITLE OF INVENTION: and recombinant DNA for use therein

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Morrison & Foerster LLP
STREET: 2000 Pennsylvania Avenue, N.W.
CITY: Washington

STATE: DC

COUNTRY: United States of America

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,725

FILING DATE: 23-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: EP 95203620.0

FILING DATE: 22-DEC-1995

APPLICATION NUMBER: EP 96200943.7

FILING DATE: 11-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: E. Victor Donahue

REGISTRATION NUMBER: 35,492

INFORMATION FOR SEQ. ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 141 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-091-725-51

Query Match 10.2%; Score 6; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 TFGKKK 53
Db 7 TFGKKK 12

RESULT 28

US-08-871-732A-1
Sequence 1, Application US/08871732A
Patent No. 6140074

GENERAL INFORMATION:

APPLICANT: O'BRIEN, TIMOTHY J.

ATTORNEY/AGENT INFORMATION:

NAME: WANG, YIN

TITLE OF INVENTION: NOVEL SH3 PROTEIN, GENE, CHIMERIC

TITLE OF INVENTION: CELLS, VECTORS AND EXPRESSION METHOD FOR PRODUCING THE NOVE

TITLE OF INVENTION: PROTEIN, ANTIBODIES AND USES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MARTIN L. MCGREGOR

STREET: 5380 WEST 34TH STREET, #345

CITY: HOUSTON

STATE: TEXAS

COUNTRY: UNITED STATES OF AMERICA

ZIP: 77092

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE 3.5 INCH 1.44 MB STORAGE

COMPUTER: IBM COMPATIBLE

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORDPERFECT 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/871,732A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:

NAME: MCGREGOR, MARTIN L.

REGISTRATION NUMBER: 29,329

REFERENCE/DOCKET NUMBER: 1-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-682-1213

TELEFAX: 713-682-5807

TELEX: NONE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 154 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

US-08-871-732A-1

Query Match 10.2%; Score 6; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 KKKKKT 29
Db 66 KKKKKT 71

RESULT 29

US-09-346-510B-1

Sequence 1, Application US/09346510B

Patent No. 6281014

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

ATTORNEY/AGENT INFORMATION:

NAME: Wang, Yinxiang

TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof

FILE REFERENCE: D6221CIP

CURRENT APPLICATION NUMBER: US/09/346,510B

CURRENT FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: 08/871,732

PRIOR FILING DATE: 1997-06-09

NUMBER OF SEQ ID NOS: 32
SEQ ID NO 1
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: amino acid sequence of TADG5 protein
US-09-346-510B-1

Query Match
Best Local Similarity 10.2%; Score 6; DB 4; Length 154;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKT 29
DB 66 KKKKKT 71

RESULT 30
US-08-533-669A-4
Sequence 4, Application US/08533669A
Patent No. 5834592
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,669A
FILING DATE: 22-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-533-669A-4

Query Match
Best Local Similarity 10.2%; Score 6; DB 2; Length 175;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AKRRMQ 37
DB 160 AKRRMQ 165

RESULT 31
US-09-183-861-4
Sequence 4, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.

APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-183-861-4

Query Match
Best Local Similarity 10.2%; Score 6; DB 4; Length 175;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AKRRMQ 37
DB 160 AKRRMQ 165

RESULT 32
US-09-022-765-4
Sequence 4, Application US/09022765
Patent No. 6375955
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/022,765
;; FILING DATE: 12-FEB-1998
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MAKI, David J.
;; REGISTRATION NUMBER: 31,392
;; REFERENCE/DOCKET NUMBER: 210121.420C3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 175 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-022-765-4

Query Match 10.2%; Score 6; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 AKRRMQ 37
Db 160 AKRRMQ 165

RESULT 33
US-08-468-347-24
; Sequence 24, Application US/08468347
; Patent No. 5783421
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,347
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

;; FRAGMENT TYPE: N-terminal
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..197
;; US-08-468-347-24

Query Match 10.2%; Score 6; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 KKKKKT 29
Db 191 KKKKKT 196

RESULT 34
US-08-467-389-24
; Sequence 24, Application US/08467389
; Patent No. 5824641
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,389
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..197
;; US-08-467-389-24

Query Match 10.2%; Score 6; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 KKKKKT 29
Db 191 KKKKKT 196

```
RESULT 35
US-08-779-379-24
; Sequence 24, Application US/08779379
; Patent No. 5858970
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,379
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPM/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..197
US-08-779-379-24

Query Match          10.2%; Score 6; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 24 KKKKKT 29
Db 191 KKKKKT 196

```
RESULT 36
US-08-469-219-24
; Sequence 24, Application US/08469219
; Patent No. 5863534
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
```

```
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,219
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPM/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..197
US-08-469-219-24

Query Match          10.2%; Score 6; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 24 KKKKKT 29
Db 191 KKKKKT 196

```
RESULT 37
US-09-228-152-24
; Sequence 24, Application US/09228152
; Patent No. 6211341
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa INHIBITORY ACTIVITY
; FILE REFERENCE: 43020aYa
; CURRENT APPLICATION NUMBER: US/09/228,152
; CURRENT FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Deduced amino
; OTHER INFORMATION: acid sequence of clone pSP65-Xa1-13.
US-09-228-152-24
```

Query Match 10.2%; Score 6; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKT 29
DB 191 KKKKT 196

RESULT 38

US-08-903-801-3
; Sequence 3, Application US/08903801
; Patent No. 5932712
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/903,801
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; FILING DATE:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0354 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1514949
US-08-903-801-3

Query Match 10.2%; Score 6; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKT 29
DB 217 KKKKT 222

RESULT 39
US-09-295-055-3
; Sequence 3, Application US/09295055
; Patent No. 6232440
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer
; APPLICANT: Corley, Neil C.

APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/295,055
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/903,801
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0354 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1514949
US-09-295-055-3

Query Match 10.2%; Score 6; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKT 29
DB 217 KKKKT 222

RESULT 40
US-09-149-476-568
; Sequence 568, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 166 Human secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336

EARLIER APPLICATION NUMBER:	60/056,886
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,877
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,889
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,893
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,630
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,878
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,662
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,872
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,882
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,637
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,903
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,888
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,879
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,880
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,894
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,911
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,864
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,874
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,910
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,864
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,631
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,845
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,892
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/057,761
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/047,595
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,599
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,588
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,585
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,594
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,589
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,593
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,614
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/043,578
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,576
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/047,501

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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          10.2%: Score 6; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      23 EKKKKK 28
        |||||
Db      245 EKKKKK 250

RESULT 41
US-09-347-803-20
; Sequence 20, Application US/09347803
; Patent No. 6274379
; GENERAL INFORMATION:
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hiltz, Bill
; APPLICANT: Kinney, Tony
; APPLICANT: Orozco, Buddy
; TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
; FILE REFERENCE: BB-1176
; CURRENT APPLICATION NUMBER: US/09/347,803
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,952
; EARLIER FILING DATE: July 15, 1998
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Glycine max
US-09-347-803-20
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Query Match          10.2%: Score 6; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      2 VHGSIA 7
        |||||
Db      134 VHGSIA 139
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```
RESULT 42
US-09-615-192A-389
; Sequence 389, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c40
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-615-192A-389
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Query Match          10.2%: Score 6; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      54 GPNANS 59
        |||||
Db      92 GPNANS 97
```

```
RESULT 43
US-09-347-803-16
; Sequence 16, Application US/09347803
; Patent No. 6274379
; GENERAL INFORMATION:
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hiltz, Bill
; APPLICANT: Kinney, Tony
; APPLICANT: Orozco, Buddy
; TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
; FILE REFERENCE: BB-1176
; CURRENT APPLICATION NUMBER: US/09/347,803
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,952
; EARLIER FILING DATE: July 15, 1998
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-803-16
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Query Match          10.2%: Score 6; DB 4; Length 341;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      2 VHGSIA 7
        |||||
Db      126 VHGSIA 131
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RESULT 44
US-08-729-214-27
; Sequence 27, Application US/08729214
; Patent No. 5817502
```

```

;
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Hammer, Phillip E.
; APPLICANT: van Pee, Karl-Heinz
; APPLICANT: Kirner, Sabine
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,214
; FILING DATE: TBA
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-729-214-27

Query Match          10.2% Score 6; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 10
      |||||
Db 214 SLARAG 219

RESULT 45
US-09-028-934-27
; Sequence 27, Application US/09028934
; Patent No. 6117670
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Lam, Steven T.
; APPLICANT: Hammer, Phillip E.
; APPLICANT: van Pee, Karl-Heinz
; APPLICANT: Kirner, Sabine
; APPLICANT: Young, Thomas R.
; TITLE OF INVENTION: Pyroglutinin Biosynthesis Genes and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117670artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/028,934
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1506/CIP7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-028-934-27

Query Match          10.2% Score 6; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 10
      |||||
Db 214 SLARAG 219
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Search completed: February 6, 2003, 21:32:33
Job time : 17 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 21:09:24 : Search time 35 Seconds

(without alignments)
224.622 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: *
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	59	AAK48204	Heparin-binding pr
2	59	100.0	59	AAW5381	Antimicrobial pept
3	59	100.0	66	ABP42408	Human ovarian anti
4	59	100.0	170	AAW43549	Human cancer assoc
5	41	69.5	41	AAW03681	Long term potentia
6	39	66.1	108	ABG27228	Novel human diagno
7	39	66.1	108	ABG27519	Novel human diagno
8	37	62.7	40	AAO08731	Human polypeptide
9	37	62.7	157	AAG75965	Human colon cancer
10	32	54.2	130	AAG01569	Human secreted pro

ID	AAK48204	standard; protein; 59 AA.	ALIGNMENTS
11	32	54.2	312 22 AAU30872 Novel human secret
12	31	52.5	61 22 ABG27230 Novel human diagno
13	31	52.5	90 22 ABG27520 Novel human diagno
14	28	47.5	118 22 ABB29449 Peptide #2100 enco
15	28	47.5	118 22 ABB34625 Peptide #2131 enco
16	28	47.5	118 22 ABB20035 Protein #2034 enco
17	28	47.5	118 22 AAM55415 Human brain expres
18	28	47.5	118 22 AAM67811 Human bone marrow
19	28	47.5	118 22 AAM15620 Peptide #2054 enco
20	28	47.5	118 22 AAM28118 Peptide #2155 enco
21	28	47.5	118 22 AAM03364 Peptide #2046 enco
22	28	47.5	118 23 ABG37354 Human peptide enco
23	24	40.7	35 22 AAO07113 Human polypeptide
24	22	37.3	62 21 AAG04311 Arabidopsis thalia
25	22	37.3	62 21 AAG15348 Arabidopsis thalia
26	22	37.3	62 21 AAG22753 Arabidopsis thalia
27	22	37.3	62 21 AAG32888 Zea mays protein f
28	22	37.3	62 21 AAG34119 Zea mays protein f
29	22	37.3	62 21 AAG38861 Arabidopsis thalia
30	22	37.3	62 21 AAG39476 Arabidopsis thalia
31	22	37.3	62 21 AAG40704 Zea mays protein f
32	22	37.3	62 21 AAG40788 Zea mays protein f
33	22	37.3	62 21 AAG44883 Zea mays protein f
34	22	37.3	62 21 AAG48690 Arabidopsis thalia
35	22	37.3	68 21 AAG31871 Arabidopsis thalia
36	22	37.3	82 21 AAG40703 Zea mays protein f
37	22	37.3	83 21 AAG44882 Zea mays protein f
38	22	37.3	84 21 AAG32887 Zea mays protein f
39	22	37.3	93 21 AAG34118 Zea mays protein f
40	22	37.3	110 21 AAG32886 Zea mays protein f
41	22	37.3	130 21 AAG26788 Zea mays protein f
42	21	35.6	230 23 ABG34132 Human sebB protel
43	21	35.6	459 23 ABG34132 Human sebB protel
44	20	33.9	65 21 AAG20231 Arabidopsis thalia
45	19	32.2	229 22 AAU31057 Novel human secret

RESULT 1
ID AAK48204
AAK48204; standard; protein; 59 AA.
12-JUL-1994 (first entry)
Heparin-binding protein.
Cell growth agent; wound; bone disease; treatment; treating; agent.
Rattus norvegicus.
JP05339287-A.
21-DEC-1993.
05-JUN-1992; 92JP-0145125.
05-JUN-1992; 92JP-0145125.
05-JUN-1992; 92JP-0145125.
(FARH) HOECHST JAPAN LTD.
WPI; 1994-031824/04.
New heparin-binding protein - used as a cell growth agent for
treatment of wounds and bone disease
Claim 1; Page 3; App; Japanese.
The sequence is that of a heparin binding-protein which is useful as
a cell growth agent and in the treatment of wounds and bone disease.

XX Sequence 59 AA;
 SQ
 Query Match 100.0%; Score 59: DB 15: Length 59:
 Best Local Similarity 100.0%; Pred. No. 1.9e-54;
 Matches 59: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVGSLARAGKVGQTPPKVAKOEKKKKKTGRARRMQYNRRFVNVVPTFGKKKGPNANS 59
 Db 1 KVGSLARAGKVGQTPPKVAKOEKKKKKTGRARRMQYNRRFVNVVPTFGKKKGPNANS 59

RESULT 2
 AAW95381
 ID AAW95381 standard; peptide: 59 AA.
 XX
 AC AAW95381:
 XX
 DT 17-MAR-1999 (first entry)
 XX
 DE Antimicrobial peptide fragment from ubiquitin.
 XX
 KM ubiquitin; treatment: diagnosis; prophylaxis; infection; microbial;
 KM pathogenic; Gram-positive bacteria; antimicrobial; Staphylococcus aureus;
 KM listeria monocytogenes; Gram-negative; Klebsiella pneumoniae; E. coli;
 KM enterococcus; Salmonella typhimurium; Mycobacterium avium; M. fortuitum;
 KM fungus; Candida albicans; Cryptococcus neoformans; Aspergillus fumigatus;
 KM virus; parasite; Trypanosoma cruzi; Toxoplasma gondii.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN WO9854314-A1.
 XX
 PD 03-DEC-1998.
 XX
 PE 29-MAY-1998: 98WO-NL00311.
 XX
 PR 29-MAY-1997: 97NL-1006164.
 XX
 PA (UYLE-) RICKSUNIV LEIDEN.
 XX
 PI Feltma RIJ, Hienstra PS, Nibbering PH, Pauwels EKJ;
 PI Van Den Barselaar MT;
 XX
 DR WPI: 1999-070214/06.
 XX
 PT New antimicrobial peptides derived from ubiquitin - useful for
 PT the prophylaxis, diagnosis and treatment of infections in humans and
 PT animals
 XX
 PS Claim 2: Page 23; 48pp; English.
 XX
 CC Sequences AAW95381-389 represent antimicrobial peptide fragments derived
 CC from ubiquitin. Ubiquitin or optionally modified peptide fragments
 CC of ubiquitin, may be used for the treatment, diagnosis, or
 CC prophylaxis of infections in humans and animals. In particular the
 CC products and methods are directed against microbial infections caused by
 CC pathogenic Gram-positive Staphylococcus aureus, including antibiotic
 CC resistant strains, listeria monocytogenes, and Gram-negative antibiotic
 CC resistant Klebsiella pneumoniae, E. coli, enterococci, and Salmonella
 CC typhimurium bacteria, micro-organisms difficult to treat such as
 CC Mycobacterium avium and M. fortuitum, fungi such as Candida albicans,
 CC Cryptococcus neoformans, and Aspergillus fumigatus, viruses, in
 CC particular enveloped viruses, and parasites such as Trypanosoma cruzi and
 CC Toxoplasma gondii.
 CC
 SQ Sequence 59 AA;
 XX
 Query Match 100.0%; Score 59: DB 20: Length 59:
 Best Local Similarity 100.0%; Pred. No. 1.9e-54;
 Matches 59: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVGSLARAGKVGQTPPKVAKOEKKKKKTGRARRMQYNRRFVNVVPTFGKKKGPNANS 59
 Db 1 KVGSLARAGKVGQTPPKVAKOEKKKKKTGRARRMQYNRRFVNVVPTFGKKKGPNANS 59

RESULT 3
 ID ABP42408
 ID ABP42408 standard; Protein: 66 AA.
 XX
 AC ABP42408:
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HOCM79, SEQ ID NO:3540.
 XX
 KM Human: ovarian antigen; ovary; ovarian: breast; cancer; tumour;
 KM ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KM PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KM inflammatory condition; immune disorder; blood disorder;
 KM cardiovascular disorder; respiratory disorder; neurological disorder;
 KM gastrointestinal disorder; urinary system disorder; drug screening;
 KM gene therapy; chromosome mapping; forensic analysis;
 KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KM antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 OS
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001: 2001WO-US18569.
 XX
 PR 07-JUN-2000: 2000US-209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 PI WPI: 2002-147878/19.
 DR N-PSDB: AB055485.
 XX
 DR Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 DR useful in the prevention, treatment and diagnosis of cancer (e.g.
 PT ovarian cancer), immune disorders, cardiovascular disorders and
 PT neurological diseases -
 XX
 PS Claim 11: SEQ ID NO 3540; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 CC encompasses polypeptides 908 identical and polynucleotides 958 identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prophylaxis or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the

polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present CC sequence represents a human ovarian antigen of the invention. CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at [ftp://wipo.int/pub/publ/published_pcl_sequences](http://wipo.int/pub/publ/published_pcl_sequences).

XX Sequence 66 AA;

Query Match 100.0%; Score 59; DB 23; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.1e-54;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHGSLARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKGPNNNS 59
DB 8 KHGSLARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKGPNNNS 66

RESULT 4
AAB43549

ID AAB43549 standard; Protein; 170 AA.

AC AAB43549;

DT 08-FEB-2001 (first entry)

XX Human cancer associated protein sequence SEQ ID NO:994.

DE Human cancer associated protein sequence SEQ ID NO:994.
XX Human: Cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerability; immunomodulator;
KM antidiabetic; antiallergic; antipneumatic; antiarthritic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; neutropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KM allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KM neurological disease; drug screening.

XX Homo sapiens.

OS WO200055350-A1.

PN 21-SEP-2000.

PD 08-MAR-2000; 2000WO-US05882.

PF 12-MAR-1999; 99US-0124270.

PR (HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Ruben SM;

XX WPI: 2000-587533/55.

DR N-PSDB; AAC77758.

PT Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer -

PS Claim 11; Page 1568-1569; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given
CC in AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerability; immunomodulator;
CC antidiabetic; antiallergic; antipneumatic; antiarthritic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC neutropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating

or inhibiting the proliferation, differentiation or mobilisation of CC immune cells, to treat disorders of haematopoietic cells, autoimmune CC disorders, allergic reactions, graft versus host disease and organ CC rejection, modulate haemostatic or thrombolytic activity, modulate CC inflammation, cancers, cardiovascular disorders, neurological disease and CC bacterial or viral infections. The peptides, nucleotides, antibodies, CC agonists and antagonists may be also be used in drug screens. AAC78449 to CC AAC78457 and AAB44240 represent sequences used in the exemplification of CC the present invention.

XX Sequence 170 AA;

Query Match 100.0%; Score 59; DB 21; Length 170;
Best Local Similarity 100.0%; Pred. No. 4.7e-54;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHGSLARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKGPNNNS 59
DB 112 KHGSLARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKGPNNNS 170

RESULT 5
AAW03681

ID AAW03681 standard; peptide; 41 AA.

AC AAW03681;

DT 31-DEC-1996 (first entry)

XX Long term potentiation inducing peptide.

DE Long term potentiation inducing peptide.
XX Long term potentiation inducing peptide; mouse; brain; senile dementia;
KW cerebrovascular; Alzheimer's disease.
KM Mus musculus.

OS JP08176193-A.

PN 09-JUL-1996.

PD 23-DEC-1994; 94JP-0336143.

PF 23-DEC-1994; 94JP-0336143.

PR (SOSE-) SOSEI KK.

PA WPI: 1996-368226/37.

DR A long-term potentiation inducing peptide - useful for the diagnosis
XX and treatment of senile dementia

PT Claim 1; Page 6; 7pp; Japanese.

PS This is the sequence of a long term potentiation inducing peptide
XX isolated from mice brains by centrifugation, extraction, dialysis

CC reverse phase HPLC and gel filtration chromatography (Sephadex C-25).

CC The peptide is useful for diagnosis and treatment of senile dementia
CC e.g. cerebrovascular or Alzheimer's dementias.

XX Sequence 41 AA;

Query Match 69.5%; Score 41; DB 17; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.1e-35;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHGSLARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRR 41
DB 1 KHGSLARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRR 41

RESULT 6
ABG27228
ID ABG27228 standard; Protein; 108 AA.

```
XX AC ABG27228;
XX XX
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #27219.
XX KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Dermanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR N-PSDB; AAS91415.
XX XX
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 20; SEQ ID NO 57587; 103pp; English.
XX XX
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX SQ Sequence 108 AA;
XX XX
XX Query Match 66.1%; Score 39; DB 22; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-33;
XX Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 20 AKOEKKKKKTGAKRRMQRNRRFVVNVPFGKKKGPNN 58
DB 69 AKOEKKKKKTGAKRRMQRNRRFVVNVPFGKKKGPNN 107
```

```
RESULT 7
ABG27519
ID ABG27519 standard; Protein; 108 AA.
XX
XX AC ABG27519;
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```
XX XX
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #27510.
XX KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Dermanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR N-PSDB; AAS91706.
XX XX
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 20; SEQ ID NO 57878; 103pp; English.
XX XX
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX SQ Sequence 108 AA;
XX XX
XX Query Match 66.1%; Score 39; DB 22; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-33;
XX Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 20 AKOEKKKKKTGAKRRMQRNRRFVVNVPFGKKKGPNN 58
DB 69 AKOEKKKKKTGAKRRMQRNRRFVVNVPFGKKKGPNN 107
```

```
RESULT 8
AAO08731
ID AAO08731 standard; Protein; 40 AA.
XX
XX AC AAO08731;
XX
XX DT 06-NOV-2001 (first entry)
```

XX Human polypeptide SEQ ID NO 22623.
DE
XX
KM Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
KM nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PP 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT.
XX
DR WPI: 2001-514838/56.
DR N-PSDB; AA188662.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders.
XX
PS Claim 20; SEQ ID NO 22623; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 40 AA;
XX
Query Match 62.7%; Score 37; DB 22; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 EKKKKKTGRAKRRMQYRRFVNVPTFGKKKGPANNS 59
Db 4 EKKKKKTGRAKRRMQYRRFVNVPTFGKKKGPANNS 40
XX
RESULT 9
AAG75965
ID AAG75965 standard; Protein: 157 AA.
XX
AC AAG75965;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:6729.
XX
KM Human: colon cancer; colon cancer antigen; diagnosis; detection;
KM colorectal carcinoma; chromosome 11.
XX
OS Homo sapiens.
XX

PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PP 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA.
XX
DR WPI: 2001-235357/24.
DR N-PSDB; AAH35370.
XX
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 11; Page 8192-8193; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing P.
CC Inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 157 AA;
XX
Query Match 62.7%; Score 37; DB 22; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.7e-31;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVNGLARAGKVRGOTPKVAKOEKKKKKTGRAKRRMQ 37
Db 106 KVNGLARAGKVRGOTPKVAKOEKKKKKTGRAKRRMQ 142
XX
RESULT 10
AAG01569
ID AAG01569 standard; Protein: 130 AA.
XX
AC AAG01569;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 5650.
XX
KM Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KM gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX

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PR 26-FEB-1999; 9905-0122487.
XX
XX (GEST ) GENSET.
XX
XX Dumas Mline Edwards J, Duclert A, Giordano J;
XX WPI: 2000-500381/45.
XX N-PSDB: AAC01575.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 13; SEQ ID 5650; 71pp + CD-ROM; English.
XX
CC The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30
CC different tissues. EST sequences usually correspond mainly to the 3'
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.
XX
XX Sequence 130 AA:
SQ
XX
XX Query Match 54.2%; Score 32; DB 21; Length 130;
XX Best Local Similarity 100.0%; Pred. No. 8.6e-26;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYHGSLARAGKVRGQTPKVAKEKKKKKTGRA 32
DB 75 KYHGSLARAGKVRGQTPKVAKEKKKKKTGRA 106
XX
XX RESULT 11
XX AAU30872
XX ID AAU30872 standard; Protein: 312 AA.
XX AC AAU30872;
XX
XX 18-DEC-2001 (first entry)
XX
XX Novel human secreted protein #1363.
XX
XX Human: vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukemia.
XX
XX Homo sapiens.
XX
XX WO200179449-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US08656.
XX
XX 18-APR-2000; 2000US-0552929.
XX
XX 26-JAN-2001; 2001US-0770160.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI: 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy -
PT

```

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XX
XX Claim 20; Page 364; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukemias. AAU29510-AAU3304 represent the amino acid
XX sequences of novel human secreted proteins of the invention.
XX
XX Sequence 312 AA:
SQ
XX
XX Query Match 54.2%; Score 32; DB 22; Length 312;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-25;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 EKKKKKTGRAKRRMOYNRFFVNVVVFEGKKKG 54
DB 72 EKKKKKTGRAKRRMOYNRFFVNVVVFEGKKKG 103
XX
XX RESULT 12
XX ABG27230
XX ID ABG27230 standard; Protein: 61 AA.
XX AC ABG27230;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #27221.
XX
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX N-PSDB: AAS91417.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20; SEQ ID No 57589; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC

```

CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 61 AA:

Query Match 52.5%; Score 31; DB 22; Length 61;
Best Local Similarity 100.0%; Pred. No. 4.9e-25;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 29 TGRARRMQYNRRFVNVPTFGKKKGPNNNS 59
Db 31 TGRARRMQYNRRFVNVPTFGKKKGPNNNS 61
|||||
RESULT 13
ABG27520
ID ABG27520 standard; Protein; 90 AA.
XX
AC ABG27520;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #27511.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HXSE-) HXSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS91707.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID NO 57879; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 90 AA:

Query Match 52.5%; Score 31; DB 22; Length 90;
Best Local Similarity 100.0%; Pred. No. 7e-25;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 29 TGRARRMQYNRRFVNVPTFGKKKGPNNNS 59
Db 60 TGRARRMQYNRRFVNVPTFGKKKGPNNNS 90
|||||
RESULT 14
ABB29449
ID ABB29449 standard; Peptide; 118 AA.
XX
AC ABB29449;
XX
DT 01-FEB-2002 (first entry)
XX
DE Peptide #2100 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00662.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI: 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
XX Claim 27; SEQ ID NO 12417; 327bp + sequence listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids

CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC determine proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosis breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a peptide encoded by a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 118 AA;

Query Match 47.5%; Score 28; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHSLARAGKVRGOTPKVAOEKKKK 28
Db 56 KVHSLARAGKVRGOTPKVAOEKKKK 83
|||||

RESULT 15
ABB34625
ID ABB34625 standard; Peptide: 118 AA.
XX
AC ABB34625;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #2131 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human foetal liver.
XX
XX
XX Claim 27; SEQ ID NO 27260; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC foetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 118 AA;

Query Match 47.5%; Score 28; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHSLARAGKVRGOTPKVAOEKKKK 28
Db 56 KVHSLARAGKVRGOTPKVAOEKKKK 83
|||||

RESULT 16
ABB20035
ID ABB20035 standard; Protein: 118 AA.
XX
AC ABB20035;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #2034 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
XX
XX Claim 15; SEQ ID NO 21805; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosis diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 118 AA;

Query Match 47.5%; Score 28; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Feb 7 08:54:57 2003

OY 1 KVHSLARAGKVRGQTPKVAKEKKKK 28
 |||||||
 DB 56 KVHSLARAGKVRGQTPKVAKEKKKK 83

RESULT 17
 AAM55415
 ID AAM55415 standard; Protein: 118 AA.

AC AAM55415;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27520.

KW Human: brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer.

OS Homo sapiens.

PN W0200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00667.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX PI WPI; 2001-483446/52.

XX DR WPI; 2001-483446/52.

XX PT Single exon nucleic acid probes for analyzing gene expression in human

XX PS brains -

XX Example 4; SEQ ID NO: 27520; 650bp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid

XX CC probes which are derived from genomic sequences expressed in the human

XX CC brain. They can be used to measure gene expression in brain cell samples,

XX CC which may enable the diagnosis and improved treatment of nervous system

XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX CC epilepsy and cancers. The present sequence is a protein encoded by one of

XX CC the probes of the invention.

XX SQ Sequence 118 AA;

DT Query Match 47.5%; Score 28; DB 22; Length 118;
 Best Local Similarity 100.0%; Pred. No. 1.3e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVHSLARAGKVRGQTPKVAKEKKKK 28
 |||||||
 DB 56 KVHSLARAGKVRGQTPKVAKEKKKK 83

RESULT 18

AAM67811

ID AAM67811 standard; Protein: 118 AA.

AC AAM67811;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28117.
 KW Human: bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukemia; lymphoma; myeloma.

OS Homo sapiens.

PN W0200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00668.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX PI WPI; 2001-488900/53.

XX DR WPI; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for

XX PS analyzing gene expression in human bone marrow -

XX Example 4; SEQ ID NO: 28117; 658bp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid

XX CC probes which are derived from genomic sequences expressed in the human

XX CC bone marrow. They can be used to measure gene expression in bone marrow

XX CC samples, which may enable the improved diagnosis and treatment of cancers

XX CC such as lymphoma, leukemia and myeloma. The present sequence is a

XX CC protein encoded by one of the probes of the invention.

XX SQ Sequence 118 AA;

DT Query Match 47.5%; Score 28; DB 22; Length 118;
 Best Local Similarity 100.0%; Pred. No. 1.3e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVHSLARAGKVRGQTPKVAKEKKKK 28
 |||||||
 DB 56 KVHSLARAGKVRGQTPKVAKEKKKK 83

RESULT 19
 AAM15620
 ID AAM15620 standard; Protein: 118 AA.

AC AAM15620;

DT 12-OCT-2001 (first entry)

DE Peptide #2054 encoded by probe for measuring cervical gene expression.

KW Probe: human; microarray; gene expression; cervical epithelial cell;

OS Homo sapiens.

PN W0200157278-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00670.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 27; SEQ ID No 20446; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
CC (SENP: see AAI10068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 118 AA;

Query Match 47.5%; Score 28; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSILARAGKVRGQTPKVAKDEKKKK 28
DB 56 KVHGSILARAGKVRGQTPKVAKDEKKKK 83

RESULT 20

ID AAM28118 standard; Protein; 118 AA.

XX AAM28118;

DT 17-OCT-2001 (first entry)

XX Peptide #2155 encoded by probe for measuring placental gene expression.

KW Probe: microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.

OS Homo sapiens.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00663.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-48897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
XX
PS Claim 27; SEQ ID No 28387; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP;
CC see AAI13135-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
SQ Sequence 118 AA;

Query Match 47.5%; Score 28; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSILARAGKVRGQTPKVAKDEKKKK 28
DB 56 KVHGSILARAGKVRGQTPKVAKDEKKKK 83

RESULT 21

ID AAM03364 standard; Protein; 118 AA.

XX AAM03364;

DT 09-OCT-2001 (first entry)

XX Peptide #2046 encoded by probe for measuring breast gene expression.

KW Probe: human; breast disease; breast cancer; development disorder;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.

OS Homo sapiens.

PN WO200157270-A2.

PD 09-AUG-2001.

PF 29-JAN-2001; 2001WO-US00661.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-476286/51.

Novel single exon nucleic acid probe used to measuring gene expression
in a human breast -

PS Claim 27; SEQ ID No 12104; 322pp; English.

XX The present invention relates to novel single exon nucleic acid probes
CC (see AAI10010-AA110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic

XX MPI; 2001-514838/56.
DR N-PSDB; AA187044.
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX Claim 20; SEQ ID NO 21005; 1399pp + Sequence Listing; English.
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 35 AA;
Query Match 40.7%; Score 24; DB 22; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.8e-18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 MOYRRFVNVPPEGKKKGPNANS 59
DB 12 MQYRRFVNVPPEGKKKGPNANS 35
RESULT 24
AAG04311
ID AAG04311 standard; Protein; 62 AA.
XX
AC AAG04311;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 290.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128645.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 99US-0131449.

PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
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PR 14-MAY-1999; 99US-0134219.
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PR 18-MAY-1999; 99US-0134768.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 17-JUN-1999; 99US-0139492.
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PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
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PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
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PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
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PR 21-JUL-1999; 99US-0145086.
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PR 27-JUL-1999; 99US-01455918.
PR 28-JUL-1999; 99US-0145591.
PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0146389.
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PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147182.
PR 05-AUG-1999; 99US-0147260.
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PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
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PR 23-AUG-1999; 99US-0149920.
PR 23-AUG-1999; 99US-0150566.
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PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 15-SEP-1999; 99US-0154018.
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PR 04-OCT-1999; 99US-0157117.
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PR 07-OCT-1999; 99US-0158029.
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PR 21-OCT-1999; 99US-0160741.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 25-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 KVHGSARACKVRCGTPTKVAKO 22
Db 3 KVHGSARACKVRCGTPTKVAKO 24

RESULT 25
AAG15348
ID AAG15348 standard; Protein: 62 AA.
XX
AC AAG15348;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 15567.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126284.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
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PR 01-JUL-1999; 99US-0142154.
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PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.

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PR 27-JUL-1999; 99US-0145919.
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PR 02-AUG-1999; 99US-0146388.
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PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148584.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151330.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154479.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
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PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.38; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVHSLARAGKVGOTPKVAKQ 22
Db 3 KVHSLARAGKVGOTPKVAKQ 24

RESULT 26
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AC AAG22753;
XX
DT 17-OCT-2000 (first entry)
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DE Zea mays protein fragment SEQ ID NO: 25803.
XX
KM Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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PR 10-SEP-1999; 99US-0153070.
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PR 29-OCT-1999; 99US-0162142.
Query Match 37.3%; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3 KKHGSLRAGKVRGQPKYAKQ 24
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ID AACG32888 standard; Protein; 62 AA.
AC AACG32888;
XX
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 39761.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
XX EP1033405-A2.
PN
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PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
PF
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XX 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
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PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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PR 04-JUN-1999; 99US-0137502.
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PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 29-SEP-1999; 99US-0156596.
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PR 05-OCT-1999; 99US-0157753.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match

37.3%; Score 22; DB 21; Length 62;

Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 KXHGSILARAGKVRGQTPKVAQ 24

RESULT 28
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XX
XX AAG34119;
AC
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XX 18-OCT-2000 (first entry)
DT
XX
XX Zea mays protein fragment SEQ ID NO: 41466.
DE
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
XX Zea mays subsp. mays.
OS
XX
XX EP1033405-A2.
PN
XX
XX 06-SEP-2000.
PD
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XX 25-FEB-2000; 2000EP-0301439.
PF
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XX 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 28-APR-1999; 99US-0131449.
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Query Match 37.3%: Score 22; DB 21; length 62;
Best Local Similarity 100.0%: Pred. No. 1.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 KVHGSRLRAGKVRGQTPKRVAKO 24

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AC AAG38861;
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Best Local Similarity 100.0%; Pred. No. 1,4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 KKHGSLRAGKVRGOTPKVAKO 24

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AC AAG39476;
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DT 18-OCT-2000 (first entry)
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KW Protein identification: signal transduction pathway; metabolic pathway;
KM hydrolisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PM EPI033405-A2.
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PD 06-SEP-2000.
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PR	07-OCT-1999;	990S-0158029.
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Query Match      37.3%; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1,4e-15;
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RESULT 31
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XX
AC AAG40704;
XX
DT 18-OCF-2000 (first entry)
XX
DE zea mays protein fragment SEQ ID NO: 50541.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
  hybridisation assay; genetic mapping; gene expression control; promoter;
  termination sequence; corn.

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XX		66-SEP-2000.	
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PR 29-OCT-1999: 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1,4e-15;
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AC AAG40788;
XX
DT 18-OCT-2000 (first entry)
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DE Zea mays protein fragment SEQ ID NO: 50657.
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KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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Query Match 37.3%; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX AAG44883;

XX 18-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 56275.

KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

XX Zea mays subsp. mays.

XX EPI033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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PF 25-FEB-2000; 2000EP-0301439.
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ID AAG31871 standard; Protein; 68 AA.

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana prote
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KW protein identification; signal transduction pathway; metabolic pathway;
 hybridisation assay; genetic mapping; gene expression control; promoter
 identification

termination sequence.

OS Arabidopsis thaliana.
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EP1033405-A2.
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PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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DT 18-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 50540.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
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AC AAG44882;
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence; corn.
XX
OS Zea mays subsp. mays.
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PN EPI033405-A2.
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Best Local Similarity 100.0%; Pred. No. 1.8e-15;
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
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PN EPI033405-A2.
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PR 31-AUG-1999; 99US-015138.
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PR 07-SEP-1999; 99US-0152363.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKHGSLRACKVKGQTPKVAQ 22

Db 25 KVGSLRAGKVRGCTPKVAKQ 46
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RESULT 39
AAG34118
ID AAG34118 standard; Protein; 93 AA.
XX
AC AAG34118;
XX
DT 18-OCT-2000 (first entry)
DE Zea mays protein fragment SEQ ID NO: 41465.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP103405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 200EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
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PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151930.
PR 01-SEP-1999; 99US-0152363.
PR 07-SEP-1999; 99US-0153070.
PR 10-SEP-1999; 99US-0153758.
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PR 24-SEP-1999; 99US-0156458.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.38; Score 22; DB 21; Length 93;
Best Local Similarity 100.08; Pred. No. 2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHSLARAGKVRGCTPRVAKQ 22
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Db 34 KVHSLARAGKVRGCTPRVAKQ 55

RESULT 40
AAG32886
ID AAG32886 standard; Protein: 110 AA.

XX AAG32886;
AC 17-OCT-2000 (first entry)
XX
DT Zea mays protein fragment SEQ ID NO: 39759.
DE
XX Zea mays protein fragment
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
PD
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR 08-APR-1999; 99US-0128714.
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PR 19-APR-1999; 99US-0130077.
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PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
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PR 28-JUL-1999; 99US-0145951.
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PR 10-AUG-1999; 99US-0148171.
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PR 23-AUG-1999; 99US-0149930.

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PR 26-AUG-1999; 99US-0150884.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 110;
Best Local Similarity 100.0%; Pred. No. 2,4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKHGSLARAGKVRGQTPKVAQ 22
DB 51 KKHGSLARAGKVRGQTPKVAQ 72

RESULT 41

AAG26728 standard; Protein; 130 AA.

XX AAG26728;

XX 17-OCT-2000 (first entry)

DE Zee mays protein fragment SEQ ID NO: 31293.

XX

KW Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
XX
OS Zea mays subsp. mays.
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123380.
PR 09-MAR-1999; 99US-0123548.
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PR 23-AUG-1999; 99US-0149902.
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PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
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PR 31-AUG-1999; 99US-0151438.

PR 01-SEP-1999; 99US-0151930.
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PR 13-SEP-1999; 99US-0153758.
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PR 16-SEP-1999; 99US-0154039.
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PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
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PR 13-OCT-1999; 99US-0159294.
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PR 18-OCT-1999; 99US-0159584.
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PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161933.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKHGSLRAGKVRGQTPKVAQ 22
DB 71 KKHGSLRAGKVRGQTPKVAQ 92

RESULT 42
ABG34133

ID ABG34133 standard; Protein; 230 AA.

AC ABG34133;

DT 15-JUL-2002 (first entry)

DE Human seb4B protein.

KW Tax interacting protein clone 2; TIP-2; GIPC; antigen; tumour;
KW breast cancer; prostate cancer; monoclonal antibody; 27.B1; 27.F7;
KW thyroid cancer; tetanus toxin; infection; HIV; hanta virus; Ebola;
KW human immunodeficiency virus infection; enzyme dysfunction;
KW hormone dysfunction; autoimmune disease; lupus; rheumatoid arthritis;
KW immune dysfunction; septicemia; human.
XX

OS Homo sapiens.
XX
PN WO200222851-A2.
XX
PD 21-MAR-2002.
XX
PF 18-SEP-2001; 2001WO-US29242.
XX
PR 18-SEP-2000; 2000US-0664958.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Trakht I, Canfield R, Kalantarov G, Rudchenko S;
XX
DR WPI: 2002-362353/39.
XX
PT N-PSDB; ABK70029.
XX
PT New monoclonal antibody which specifically binds and forms complex with
XX TIP-2 antigen located on surface of human cancer cells, useful for
XX diagnosing and treating cancer in a human subject -
XX
XX Example 6; Fig 41B; 276pp; English.

XX The invention relates to a monoclonal (mab) antibody which specifically
XX binds and forms a complex with TIP-2 (Tax interacting protein clone 2,
XX also known as GIPC) antigen located on the surface of human cancer cells,
XX where mab binds to the same antigen as monoclonal antibody 27.B1
XX or 27.F7 produced by hybridoma 27.B1 or 27.F7 of ATCC Designation No.
XX PTA-1599 or 1598, respectively. The mab is useful for detecting TIP-2
XX antigen bearing cancer cells, for diagnosing cancer in a subject by
XX detecting TIP-2 antigen-bearing cancer cells, for in vivo diagnosis of
XX cancer in a subject, for delivering exogenous material to TIP-2 antigen-
XX bearing cancer cells of a human subject, for treating cancer in a human
XX subject, for inducing apoptosis of a tissue section from a tumour sample
XX for the presence of TIP-2 antigen bearing cancer cells, for detecting the
XX presence of TIP-2 antigen in biological fluid, and for monitoring the
XX progression of cancer, where the cancer cells are TIP-2 antigen-bearing
XX cancer cells, in a subject. A composition comprising the mab is useful
XX for treating or preventing a condition in a subject who previously
XX exhibited the condition, where the condition is associated with cancer
XX (thyroid, breast or prostate cancer), tumour (benign), toxin (tetanus,
XX anthrax, botulinum, snake venom or spider venom), infectious agent (such
XX as Hanta virus, HTLV (not defined) I, HTLV II, Human immunodeficiency
XX virus, HIV herpes virus, influenza, Ebola, human papilloma virus,
XX Staphylococcus, Streptococcus, Klebsiella, Escherichia coli, anthrax or
XX Cryptococcus), enzyme dysfunction (hyperactivity or overproduction of the
XX enzyme), hormone dysfunction (hyperactivity or overproduction of the
XX hormone), autoimmune disease (lupus, thyroiditis, graft versus host
XX disease, transplantation rejection or rheumatoid arthritis), immune
XX dysfunction (CD3 or CD4 mediated), viral antigen, bacterial antigen,
XX eukaryotic antigen, rejection of a transplanted tissue, or the condition
XX is septicemia, sepsis, septic shock, viraemia, bacteraemia, fungaemia.
XX The present sequence is an additional human cancer associated marker
XX which can be used in the production of monoclonal antibodies.

Sequence 230 AA:

Query Match 35.6%; Score 21; DB 23; Length 230;
Best Local Similarity 100.0%; Pred. No. 5.1e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 RRMQVNRFRVNVVPTFGKKG 54
DB 1 RRMQVNRFRVNVVPTFGKKG 21

RESULT 43

ABG34132

ID ABG34132 standard; Protein; 459 AA.

AC ABG34132;

XX

PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
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PR 28-JUN-1999; 99US-0140823.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
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PR 08-JUL-1999; 99US-0142803.
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PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KVGSLRAGKVRGOTPKYA 20
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DB 3 KVGSLRAGKVRGOTPKYA 22
RESULT 45
AAU31057

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ID AAU31057 standard; Protein; 229 AA.
XX
AC AAU31057;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #1548.
XX
KM Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
XX 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT:
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy -
XX
PS Claim 20; Page 397; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of polypeptide. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Cells
XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of the polypeptide. Vectors comprising
XX the nucleic acids encoding the polypeptides and cells genetically
XX engineered to express them are also useful for producing the proteins.
XX The proteins are useful in genetic vaccination, testing and
XX therapy, and can be used as nutritional supplements. They may be used to
XX increase stem cell proliferation; to regulate haematopoiesis; and in
XX bone, cartilage, tendon and/or nerve tissue growth or regeneration;
XX CC immune suppression and/or stimulation; as anti-inflammatory agents; and
XX in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
XX sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 229 AA:

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Query Match 32.2%; Score 19; DB 22; Length 229;
 Best Local Similarity 100.0%; Pred. No. 6.4e-12;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 36 MQYNRRFVNVPTEGKKKG 54
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Db 1 MQYNRRFVNVPTEGKKKG 19

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 Job time : 37 secs

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